oshishlb

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- nucleic search, using sw model OM nucleic

Run cn:

July 7, 2004, 11:41:13 ; Search time 1883 Seconds
(without alignments)
5478.302 Million cell updates/sec

US-09-437-450A-40 Title:

Perfect score:

Sequence:

Scoring table:

3470272 seqs, 21671516995 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 6940544

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*

1: 90 ba:*
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em_sts:* em_un:*

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is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 AF301606 LOCUS DEFINITION

Caenorhabditis elegans cadmium-inducible lysosomal protein CDR-1 (cdr-1) mRNA, complete cds.
AF301606. ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Caenorhabditis elegans Caenorhabditis elegans Eukaryota, Metazoda, Nematoda, Chromadorea, Rhabditida; Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

REFERENCE AUTHORS TITLE

1 (sites) Liao, V.H. and Freedman, J.H. Cadmium-regulated genes from the nematode Caenorhabditis elegans.

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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Nov 29, 1997 this sequence version replaced gi:2546904. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-WXV-1996) Nematode Seguencing Project, Sanger
Institute, Hinton, Cambridge CBIO 15A, England and Department of
Genetics, Mashington University, St. Louis, MO 63110, USA. B-mail:
jes@sanger.ac.uk or rw@nematode.wistl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see:— http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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                                                                                                                                                                                          Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5395), 2012-2018 (1998)
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                                                                                 Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                               The C.elegans Sequencing Consortium. (bases 1 to 23602)
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/strain="Bristol N2"
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/clone="F35E8"
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                                                                                                                                   Liao, V.H.C., Dong, J. and Freedman, J.H.
Molecular Characterization of a Novel, Cadmium-inducible Gene from
Molecular Characterization of a Novel, Cadmium-inducible Gene from
The Nematode Caenorhabditis elegans. A NEW GENE THAT CONTRIBUTES TO
THE RESISTANCE TO CADMIUM TOXICITY
J. Biol. Chem. 277 (44), 42049-42059 (2002)
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ADSDLIEMRLRSHFKIPSILPTELETQSVALSKFROHHLFFVLIRFKIAVOEFYKTIIE
IIGLPTPLNPILAPLLKAIISKNYNKCQGAIGDFELSELDEILHRDLAIVENTLAKK
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                                                                                                                                                                                                                                                                                                                        Direct Submission
Submittee (30-AUG-2000) Nicholas School of the Environment, Duke
University, Box 90328, Durham, NC 27708-0328, USA
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'protein_id="AAG30870.1"
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dentification and cloning of new cadmium-responsive genes
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                            differential display
J. Bicl. Chem. 273 (48), 31962-31970 (1998)
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/evidence=experimental
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/db_xref="taxon:6239"
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18685 TICGGAIGITCICGAAAAGGACTICCCAAAGITATIGAGIAATGIGAAAGAGICICGICA 18744
                                                                   Esquence CETOGCI2.

The true right end of clone F35E8 is at 23602 in this sequence. The true left end of clone T05G11 is at 1324 in this sequence. The true right end of clone T05G12 is at 104 in this sequence. The start of this sequence (1. 104) overlaps with the end of sequence CETOGCI2. The end of this sequence (23499. .23602) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 TICGGAIGIICICGAAAAGGACTICCCAAAGTIATIGGAGTACTGTGAAAGAGTICGTCA 149
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neighbouring submissions.
The true left end of clone F35E8 is at 18616 in
                                                                                                                                                                                                                                                                                                                                                                                  organism="Caenorhabditis elegans"
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LOCUS

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/translation="MYGKGFQYPPINV2VSPVFQAFYDCIYPKLBPYKGQYKEFWFAF
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LYPKLDFFGADPAAVTNKDLYEPNTGGKYFQYAVGESGMQRSVYEKDPYKE
VKADYFFKNILLMFKTLDEWALDVBQNSYFLLDQIHRWBALDKGGLLLCQINVBLEHGI
FGEVECQMKKLLDFVWRLLDEKRYVMMKPHFVLYKKWVGFIRVFRWNVSDKECADLFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPATHTOT PLLETHSYQNNQQRAHGSQQHHTPPHQQQQMFRPDIEHGIIGAGSNSA
QQCSSTNSYIPIQTATVSIPFRNGEILHFQSFMELPNTLIDSQPIAEIFRIKNESJQD
IQQLWTECVSIFNOLCKIQPDAHDYLANIIISKLPRRYKIRIYFGREDDYLABEIL
EWRSEIQTPPIVOTHANDAEAHOYSMYVYESLQPELKNSYTGNNYQLEEIHGSSKTT
HPRRYQHHQQNOSWHTSIAERPTOQPLVBPTSEIHLASSTAVEIKNMAEKTKKVVP
TVEIPKQMCNGSRGSMTSTLLQVPSLSVLPEIIPIGLAAQQLQSEQLDEENPAMVLET
TVEIPERGREGIIPMETIISSNEIGNQIDVEDSQQLDSKOQVQKVSELQDDFIETVETKSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard name="K01D12.3"
/note="contains similarity to Pfam domain: PF01482 (Domain
of unknown function), Score=202.1, E-value=2.8e-57, N=1"
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QPPANTDEVKYVAFPKRDENITMYTLGIGHDVDAEMRLKKLR?KTFFFGVDPSPEINK
DLYEVKLGGNYFQIAVSGKGGMQKSYIFRKEYRDEATWHIGADYFFGDMLQKPRVDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIGHPWDEGTOORYQLAPRIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'tränslation="MFSIKSVIANIETSFQVRQSTQKRRRWQTNQHLCQSMQSEITKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILTLILTINCSEKNHQKPVQVQPKQPLHRLRLQPQPHQNLLQHLPQPLESTNTRSRR
                                                                                                                      MODIEGNEEPVLDMIHRGGFLOGRGYTICGMNIBIHKDIMKDITGEREKFHDFVWKLL.
ADKKYIMVKPPYVYWFHQPIRTVIINVADPECTNLYMN"
translation="MITSMPYNRLREAILHKRKLSKHILVAMVLISSMLLLINIMQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(11177. .1144,11518. .11592,11643. .11801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MHKSRSPDQVDYPPFPVSVLSTDSIVPECNINSTTQDSVPQYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jōin(8020. .8048,8312. .8399,8466. .8585,8629. .8697,
8747. .8888,8932. .9314}
/gene="K01D12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(8020, .8048,8312, .8399,8466, .8585,8629.
8747, .8888,8932, .9314)
/gene="KOlD12.3"
                                                                                                                                                                                                                                                                                                                 /standard_name="KO1D12.2"
/fore="cDN" BST yk2el1.3 comes from this gene
cDNA BST yk2el1.5 comes from this gene
cDNA BST yk2el1.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CINA BST ykl6599.3 comes from this gene CINA BST yk2667.3 comes from this gene CINA BST yk2667.3 comes from this gene CINA EST yk26189.3 comes from this gene CINA EST yk21812.3 comes from this gene CINA EST yk11811.3 comes from this gene CINA EST yk21669.5 comes from this gene CINA EST yk2669.5 comes from this gene CINA EST yk27812.5 comes from this gene CINA EST yk21811.5 comes from this gene CINA EST yk411811.5 comes from this gene CINA EST yk552911.3 comes from this gene CINA EST yk552911.3 comes from this gene
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/protein_id="CAA99878.2"
                                                                                                                                                                                       complement (join (6025. .7139,7192. .7646))
                                                                                                                                                                                                                                                      complement (join (6005. .7139,7192. .7646))
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codom_start=1
/prodomic="Mypothetical protein K01D12.2"
/protein_id="CAA98670.1"
/db_xref="G1:3878144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein K01D12.3"
/protein_id="CAA99877.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(9968. .10033,10136. .10426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .10033,10136. .10426)
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/standard_name="K01D12.15"
/note="cDNA_EST_yk16399.5 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="GI:14530514"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db xref="GI:3878151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="K01D12.15"
oin(9968. .10033
                                                                                                                                                                                                                           /gene="K01D12.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlap between neighbouring submissions.
This sequence is the entire insert of clone KOID12. The true right end of clone F23H12 is at 4908 in this sequence. The start of this sequence (1. .102) overlaps with the end of sequence 374472.
The end of this sequence (32761. .36974) overlaps with the start of
                18745 IGAAGTTIACCCAAAGGACTITACTAIGIGAATTAAAITGICAAACTAGIAGTCAGATCA 18804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                linear INV 10-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-JUN-1996) Nematode Sequencing Project, Sanger Institute, Hinkton, Cambridge CBIO 158, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Mashington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1318,1365. .1564,1640. .1828,1874. .2015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .1318,1365. .1564,1640. .1828,1874. .2015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                CEKO1D12 36974 bp DNA linear INV Caenorhabditis elegans cosmid KO1D12, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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/protein.id="CAA99867.1"
/db_xref="G1:3878141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'standard name="K01D12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6239"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2129. ,2505)
/gene="K01D12.1"
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/gene="K01D12.1"
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                                                                                                                                             18805 ATAMATTTACGTGG 18820
                                                                                                                                                                                                                                                                                                                                                                                                                          HTG, Potassium channel
Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 36974)
                                                                                                                                                                                                                                                                                                                                                                                                   Z75543.1 GI:1418539
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                                                                                  ATAAATTCTACGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join (1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oin (1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      name=K01D12
IMPORTANT:
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                                                                                     210
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                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                         RESULT 3
CEKOID12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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comes from this gene

.8697,

180

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sequence CEF28C1.
The true left end of clone F28C1 is at 40353 in this sequence. The true right end of clone K01012 is at 4214 in this sequence. The start of this sequence (1. .4214) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The end of this sequence (40353. .40450) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                INV 03-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute, Hinxton, Cambridge CB10 18A, England and Department of Genetics, Mashington University, St. Louis, MO 63110, USA. E-mail: jessanager.ac.uk or rwenematode-wastl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone C54D10. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note: For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                         34736 CTACAGTACTGTGAAAGAAACGAAAGGAAATTTATCCAAATGATTTACTATTTGA 34680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone C54D10 is at 1 in this sequence. The true right end of clone C54D10 is at 1020 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  available information.
Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-JUN-1996) Nematode Sequencing Project, Sanger
                                                                                                                         124 TIGGAGIACTGIGAAAGAGTICGICAIGAAGIITTACCCAAAGGACIITIACIAIGIGA
                                                                                                                                                                                                                                                                                                                                                                                       CEC54D10 40450 bp JNA linear INV Caenorhabditis elegans cosmid C54D10, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.elegans Sequencing Consortium.
2 (bases 1 to 40450)
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/strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z75531.1 GI:1418465
HTG: Serine protease inhibitor.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6239"
/clone="C54D10"
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TITLE
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CGGHMJWRRESYKVEFILESMCLVLITASAGIYSVDRMNYTJGLINNEDFNIGS
GDVVSROQOVTBMSPDLYREVPELLIGACFFYCLSNVSIVVRQLINNMIKKMDVK
GDNSELCERKKRRYRGLGLARPKGISALAGDRCCIEHLNVFRIRYDI
JGIN (21543. 22227,22273. 22400)
/gene="KQ1D12.5"
jGIN (21543. 22227,22273. 22400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREEDING AND ALTERNATION OF THE SERVICE SERVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cränslation="vhklopargigoremirantlesitrakvgcearlriyeenarf
Vliciilivylafgailfhwlewenevderlaidnrmadyokvyckekflnbcdfeem
Vrfisdgatsgllnsrsrphlgslffsatvistigfgtstrthlgrfitvygvvg
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|db_krdf="GL4617517"
|kranslation="MTSYLMGSLEGGIKANBIITKRTVLSVAAGIGIGIVFANFVRYM
RQKREAKVPQSIIEEIGKDADIIVPSAPSLRRSQSGRGMRPPSSQGERSSLRNSIRQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACDIDDIDFYSDANLDXNELRFLDGGMQAALNGBVXYRKSRNEFCKCDSETDFAAK
LYCYRQALTNALKDEHKRVWLAKCGRTJLADFIRHTKQDPVKFRNAYDEMLEYVSNDR
NEEQLRQDVEGRGVCETGFYDVAIDFIILDAFEDLKSPPSAVYSVTKNYFNSMSWKYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fprotein id="CAA99872.2"
/db xref="G1:31441821"
/translation="MGRQGSLALLLSIILIGETIANEYDGLSSHQSHQSTVTSAPIHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQQTSRNRPYNQPQLQQKESVLTQSYQVLPBSRNYYQYPQYLFTHTGYSNLQTVGQP
YQMYGSAPGSNVVSGGNSESYGYNQQAPVPTVAPAPVHFSBRQRSYSAAPTPBSPFSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(22649. .22801,22850. .23341,23437. .23753,
23798. .24207,24280. .24377,24429. .24458)}
/gene="KOlD12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQRSMNPIEADITSGQELCTELRKTIEKVHHNLENVKNRSSKOMERSIKIEGILKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVEDEIVLLVPQMEDFRDDNMEFYSVSGGSGYAGSVRTGRSRTLSVLSDDSFRSAVEE
                                                                                                 complement (join(11177. .11444,11518. .11592,11643. .11801,
11987. .12085,12159. .12481,13776. .13919,14219. .14302))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TITITITITIGSGAGGAAATCACGGCGGCGGAGGCAGCACTTCTCTCAATTGGCAACT 63
                        .12085,12159. .12481,13776. .13919,14219. .14302})
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                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="C. elegans TWK-14 protein {corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name="XO1D12.5"
/note="cDNA EST OSTF168B6 1 comes from this gene
cDNA EST OSTR168B6 1 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA 3ST YX884fl.3 comes from this gene th SST YX884fl.3 comes from this gene th SST YX1046e01.5 comes from this gene TA EST YX1046e01.3 comes from this gene TA EST YX1046e1.3 comes from this gene TA EST OSTR196H4.2 comes from this gene TA EST OSTR196H4.2 comes from this gene.
                                                                                                                                                                                                                                                  /note="similar to potassium chance protein cDNA EST yk743d10.5 comes from this gene cDNA EST yk743d10.3 comes from this gene"
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note="cDNA EST cm14g6 comes from this gene
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/product="Hypcthetical_protein K01D12.6"
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'product="Hypothetical protein K01D12.5"
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0; Mismatches 5
                                                                                                                                                                                                                          name="K01D12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA99871.1"
/db_xref="GI:3878145"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence K01D12.4
                                                                                                                                                                                     /gene="twk-14"
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Score 95.4; DB 3; Length 40450; Pred. No. 8e-15;

40.18;

Query Match Best Local Similarity

ORIGIN

34856 TATTITATTIGGAGACCACATIGCTCCAGTIGATGCGACGCTTTTIAGCCAGTIGGCAGTT 34797

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64 GICIALTAICCATTCCGCAAICACAITTCGGAIGTICICGAAAAGGACITCCCAAAGITA 123

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/translation="modekvppptyrpgociygarsynnyymrpovstarmiyrt
pmmapptmtppimtppimtppmyppiipsqpfmgpsmyspimsppmipsqpfmgpsm
vspgygytpmiavppstnvkxyd"
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FPTLVATELGEDDI PKYQUAILILLACY ENBENZE BENZADLSKI DEPETLAKLIN
LIT QNILKOHNE PEQQYED PHIGHVER PEGYL SGWYYG PKYVQPLE PETGSSLALIY
ELFYQNOHFYNML VKGGL PFANGGENGST CPDI I KQFFSFCAYLASDAQKDLKTI YSR
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PIKCNLKGKISMDVHQSAVDCIHRIVSYKKKTLNRLPPYKWSELMSALFSLISMVSTLK
ISNDXIQLNQSIHVGISTVNIFMLFINYGDSFLPSPNDYDELFYEIIRSGQVIEKFYQ
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GNNNNNNEQDNDLQEKEQNELSDDSDVEGFEIIPNNNIYSHDVSLCEPIDLVCKVTL
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KIGASLAVDSNSLTKLGICFYYGRGYTIDYNBAYRLFYQSSICDHHQBHNPEITFYYL
GLCLFYGRGYLKNQCKGFEYFMKSASLAHYSPALEAVGRCFLNGEGISQNFMQAKLYF
TTAKSGGSNQDRNIQDVNKIIBLNKSIKIKSPNILIEIEKIINENKSFNLEQSCLMYI
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QLINIRSIVQHFTSKLEEWSANNAEVALTAPQVSKIIKONYDTLRLKLQENLDQFEPY
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                                                                                                                                                                                                                                                                                                                    /translation="mockithnekknimmcinctriccydciefdhfghniksffknidkf
HCPTHDBPIIKYCILCNCVICNLCEKTTHFHNNNNQINITQFPWIPKKKSKSIBLEL
                                                                                                                                                                                                                                                                                                                                                                     NEI DEYNNYNNI NKNNNNNKNNYNNYNNYNNENKEI NEI HENHKNORSKSPPPLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein id="mAO5221.1"
(db_xref="G1:28829706"
/translation="MEIDKAVEQSSNKVEYNQPKSPITSILVNNNSSKKNNNSNNKNN
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AQCILGSSYYYGMGYSVNFEKSIKYITKSARQMRAKAYFELFNYYKQOKKDLIKSKY
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50.22 - GSCJ ID dd_02577"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="GeneID exon scores (in order of location ranges): 117.93 - GSCU ID dd_03414" (codon_start=1
                                                                                                                       2839. .4479 \note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="GenelD exon scores (in order of location ranges):
34.62, 63.42, 31.78, 100.55 - GSCJ_ID dd_01261"
/codon_start=1
/product."hypothetical_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="similar to Plasmodium falciparum. Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join (4673. .5239, 5354. .6118, 6205. .6621,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHQKNYYKQEIDNTNIKNIKCKQDSLIDKTFNKVNYLN"
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                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAO52220.1"
/db_xref="GI:28829705"
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protein id="AAM34303.2"
/db_xref="G1:28829708"
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/db_xref="GI:28829707"
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Dictyostellum discoideum chromosome 2 map 6357117-6445670 strain
                                                                                                      2096 TATTITATTI GGAGACCACATTGCTCCAGTTGATGCGACGGTTTTTAGCCAGTTGGCAGTT 2037
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Eukaryota; Mycetozoa; Dictyostellum.
1 (bases I to 88549)
2 (Gloeckner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baungart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany on Mar 4, 2003 this sequence version replaced gi:20042934. CDS predictions from GeneID do not necessarily reflect true genes. Further Information is available from IMB Jena, Department of
                                                                                                                                                          64 GTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="GeneID exon scores (in order of location ranges): 27.07 - GSGJ ID dd_01259" /codon_start=1
                                                      4 TITITITITIGGGAGGAAATCACGGCGGCGGGTGCAACAGTCTTCTCTCTAATTGGCAACT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79-85 (2002)
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Biotechnology, Beutenberstr. 11, Jena 07745, Germany
3 (bases 1 to 88549)
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                                                                                                                                                                                                                                                                      124 TIGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCCAAAGGACTTTACTATGTGA 180
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and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
Indels
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/mol_type="genomic DNA"
51;
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/map="6357117-6445670"
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/strain="AX4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACU22325 193057 bp DNA linear PRI 07-NOV-2001
Homo sapiens BAC clone RP11-391J13 from 4, complete sequence.
ACU22325
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Park Avenue, St. Louis, Missouri 63108, USA
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Missouri 63108, USA
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Submitted (09-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                    117 AAAGTTATTGGASTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTAT 176
                                                                                                                                                                                                    Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                              Gaps
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The sequence of Homo sapiens BAC clone RP11-391J13
Unpublished
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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      58.7%; Pred. No. 1.5; tive 0; Mismatches
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Sulston, J.E. and Waterston, R.
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Submitted (09-MAY-2001)
University, 4444 Forest
6 (bases 1 to 193057)
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Waterston, R.H.
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Best Local Similarity
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TLYNDOYSIGGLDENIEWLKVINTVQIGENQKENLLATLDNSTTIQPEDFTLITCKER
TLYNDOYSIGGLDENIEWLKVINTVQIGENQKENLLATLDNSTTIQPEDFTLITCKER
TLYNDOYSIGGLDENIEWLKVINTVQIGENGENGENSTERTRITCHERENSTYFKRETI
RPTLYNDOYSKWYTIFROYKRARYGILVANTGOLEGUSTSPERKYLTGSFLUNSTYFKRETI
RPTLYNDOXSILVYDQCSLLFVVQADEQREGITERNISTSPERGYNLEYTGSFLUNSTYFKRETI
RPTLYNTARGOGSYTYPISSENBETLGHOSTIFSRNISTSFRFOYNLEYTGSFTGYQUN
SIFISFSKFVIPTVWYGDIFLDNGSTLESHFKYPYFINTINAQGGANNLAVFOSSPY
QXSIALBETTLQFYFTKYPSFILVGGSTSFLSNISTSFRESTFRYGNISTSFROYSDDCIVRIS
SYSTEMNDYMANLWKLYPROYSGKTLGSFPYQVLTLEDIESIGFRNNNIDLSNSNS
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NVLYIKLNOGSISNLYNFOYTSKLGSFPYQVLTLEDIESIGFRNNNIDLSNSNS
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RSINEPWTATTGOQLIGGDYLNGTSGVNITFYTNORFIRENDLYSFTERSELGKRIQFFW
EIKYGDIPQTFSISELSIDSNLNGTTERPWTGRSCHIFFRESHANDSKRIPETESELGKRIQFFW
EIKYGDIPQTFSISELSIDSNLNGTTERPWTGRSCHIFFRESHANDSKRIPETESELGKRIQFFW
TYPRYMQNYTNQLINTLENDRILENNYTNYENDLYNFFTERSELGKRIQFFT
TRYNDINGRAFILDRILENNYTNYENDRYTERPRESHTYFINDNYEITSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(22686. .22743,22820. .22926,23004. .23139,2322. .23558,
23639. .27180)
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                                                                                                                                                                                                                                                                                                                                                            FSIAVGQCLPIBGYLSYVINDMPPTTNMFITMGGNGNSFTLKQYDSQDQWCKQDPINT
LQPDN=DTCVEQSAFINVNNSLLADTPVVYSKLFISQNVPTYADDSVIIGQYNTNTNV
CTYNDQQFGVSYTSGTVIYNENGISIHVLCNQVWQSNMFKCKESKCGETFIDTYCQXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OYARGNSFINVTIGOSOPFIESFVADIDGDLLTVNGLKFGILPTGKLRINGAIENLNI
SLPFLNNTYIVFDLKQYRNINDTNCQIYITNQLGFSSNEINFVLKAHTNVTMPFTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPTSNPTATPSLTANPTPLPTNSPSQCKNDCGGIAQGQCSNLGCICISPYIGIDCSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIVDIDPIVNNSQPEVIIPYQHENSGNKFSTLVSIYSLRELGFDGKVEKDYIFEMMNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OYYNNDNHTYFTSIKNKNDLSKRTNITVSIKMYKQLTTIQFAGENITIQPSSIKYFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSDYQFKSNLNTLDLVMYTSIETEKIDDACFSSEFGDSSSQLSSQYLKIQINDVSLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    esskienstchknosgliktoligiigstagfililivisivykksttleninra
                                                                                                                                                                                                                                                                                                                                 'ranslation="MKLLTLTLTLTLTVNYCCFINANKLFVNFWSSYSSNTCDGNPSGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSIDRYTSPVYIPTDQDILHTRVMTRGVHETNFEIGKIKFRLVDVGGQRSERKKKLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDDVTAVVECVALSEYDLLLYEDNSTRRMLESLRVFSDVCNSWFVNTPI ILFINKSBL.
FREKTKHVDLSETFPEYKGGRDYERASNYI KERFWQINKTEQNAIYSHI TCATDINNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFIKRAIVDTHIVGVLNKVRGNNINSTSNGSSSSQYISIQIPNYKTSVELDPNFSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /produčt="similar to Rhizobium loti (Mesorhizobium loti).
Dehydrogenase, succinatesemialdehyde dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="similar to Dictyostelium discoideum (Slime mold). Guanine nucleotide-binding protein alpha-2 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(27340, .29056,29330, .29490))
/note="GeneID exon scores (in order of location ranges):
218.38, 14.76 - GSCJ_ID dd_01858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(20802..21095,21199..21978)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="GeneID exon scores (in order of location ranges): 4.93, 3.57, -1.17, 18.69, 174.64 - GSCJ_ID dd_01857"
                                                                                                                                                       /note="GeneID exon scores (in order of location ranges): 57.23 - GSCJ ID dd 02576"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="hypothetical protein"
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db_xref="G1:28829711"
                                                                                                                                                                                                                                      product="hypothetical protein"
protein id="AAM34304.2"
(db_xref="G1:28829709"
                                                                                                                            complement (13151. .13840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVFEAVKDIIFTQCVMKAGLYS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'codon_start=1
                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NUSKILLONGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (G alpha 2)
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CDS

SOS

DB 3; Length 88549; Score 41;

Query Match

17.2%;

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NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we oily sequence overlapping close sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 3%; an attempt was made to resolve all sequencing problems, such a compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Prengen, B., apteno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Generals 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute http://pacpac.med.buffalo.edu]
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RPI1-627C20; the clone sequenced to the right is AC036161. Actual start of this clone is at base position 1 of RPI1-391J13; actual end is at base position 193057 of RPI1-391J13.

FEATURES

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repeat_region repeat_region

famil famil famil famil famil famil famil famil	fip5 family= fip5 family= rpt_family= f4171696 f9091893 rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family= rpt_family=	1] . 24244 6family="MEK2" 6family="MEK2" 6family="MEK2" 6family="CTAI 6family="L1" 6family="L1" 6family="L1" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="Tc2" 6family="L1" 7family="L1" 7family="L1" 7family="L1" 6family="L1" 7family="L1" 7family="L	88942896 Eppt family— Properties and the properties of the prop	ramily= 3160 3170 3170 3170 52170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 CCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 TIGGCRACIGICIATIATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /nore="clone overlaps with GenBank Accession Number AC108899 clone RP86-261015 (center project name cof)"
                  Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0:99339
Consensus quality: 138634 bases at least Q40
Consensus quality: 138674 bases at least Q30
Consensus quality: 138674 bases at least Q30
Insert size: 133000; agarose-fp
Insert size: 133683; aum-of-contigs
Quality coverage: 12.26x in Q20 bases; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC108190 clone RP86-44312 (center project name cod)"
58366. .138683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector side:left"
1. .61312
/note="clone overlaps with GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                  consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 ATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 105452 contig of 105452 bp in length 105453 105552 gap of unknown length 105553 138683: contig of 33131 bp in length.
                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 138683;
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HTG; HTGS_PHASE1; HTGS_EULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.9%; Score 40.2; DB 2;
Best Local Similarity 52.0%; Pred. No. 2.4;
Matches 90; Conservative 0; Mismatches 83;
with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .105452
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .138683
/organism="Felis catus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector side: right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RP86"
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                        52727 Greangarnakaengaentrininingakaanaengekaakentekenga
                                                                                                                                                                         52787 AACAGCCAÁTCATATATGGGGATTATÁCAATÍCCAAAATACTATTÁAAGCTATTCCTTAA 52728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC108193 138683 Dp DNA linear HTG 28-NOV-2002
Felis catus clone RP86-469M8, WORKING DRAFT SEQUENCE, 2 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Akther, N., Autonellis, A., Ayele, K., Beckstrom-Sternberg, S. M., Senjamin, B., Blakesley, R.W., Bouffard, G., Brinkley, C., Brooks, S., Carlaga, K., Coleman, B., Egle, J., Granite, S., Guan, X., Gupta, J., Eaghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, B., Larte, P., Lee-Lin, S.-C., Legaspi, R., Maduro, Q.L., Maduro, V.B., Paguirigan, C., Razson, R., Portnoy, M.E., Frasad, A., Redix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Etantripop, S., Thomas, P. U., Gruenler, M.G., Sison, C., Etantripop, S., Thomas, P. U., Guchman, J. W., Vogt, J. L., NISC, Comparative Sequencing Initiative
                                                                                                                  60 AACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAA 119
                                                                                                                                                                                                                                     120 GITATISGAGIACIGIGAAAGAGITCGICAIGAAGITIACCCAAAGGACTITACTATGIG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 138683)
                                                                                                                                                                                                                                                                                                                                                                                                           52667 TATGAATTTACAATCTTTATGAAAGTACAAAAGGGAAAGGTTGAGAACCACAA 52611
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 138683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-NOV-2002) NI: Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 28, 2002 this sequence version replaced gi:18376892.
                                                               Gaps
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      Score 41; DB 3; Length 193057; Pred. No. 1.4;
                                                            0; Mismatches 85; Indels
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Center code: NISC
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Felis catus (cat)
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      17.2%;
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                                                                                                                                                                      CLE ... Gases 1 to 22047.

RR Nale, H. Absbrokes, S. Amin, A. Angulano, D. Anglach, A. Angulano, D. Anglach, A. Angulano, D. Anglach, A. Angulano, D. Anglaches, S. Amin, A. Angulano, D. Anglacheck, S. Amin, A. Angulano, D. Anglacheck, S. Amin, A. Angulano, D. Anglachechi, V. Angulano, D. Angulachechi, V. Aoyaqi, A. Ayodeji, M. Baca, E. Baden, E. Balden, E. Balden, E. Balden, E. Balden, E. Balden, B. Barder, B. Barder, B. Barder, B. Barder, C. Greek, M. Bernel, K. Carter, A. Carter, A. Carter, A. Carter, C. Carden, G. Cherler, M. Carter, C. Carden, G. Chevland, C. Cockell, R. Carter, R. Ghard, C. Cockell, R. Carter, B. Chen, G. Chevland, C. Cockell, R. Carter, B. Chard, C. Cockell, R. Carter, C. Ding, Y. Dinh, H. Dinya, K. Dangal, C. Cockell, R. Carte, D. Ding, Y. Dinh, H. Dinya, K. Dangal, C. Cockell, R. Carte, C. Ding, Y. Dinh, H. Dinya, K. Dangal, C. Cockell, R. Carte, C. Bard, C. Bard, R. Carte, M. Carter, C. Ding, Y. Dinh, H. Dinya, K. Edgen, C. Bard, R. Carte, M. Carter, M. Garrer, D. Fernandez, S. Frisey, M. Edger, C. Bard, R. Carte, R. Garrer, P. Garra, M. Gener, R. Gill, R. Gard, A. Garrer, M. Garran, M. Garranno, E. Halland, M. Hamil C. Manilton, C. Hamilton, C. Margh, M. Marche, M. Marche, M. Marche, C. Karfe, Cl. Lebow, H. Levan, J. Logen, J. Liu, J. Liu, H. Julyk, S. Hune, J. Lawa, M. March, C. March, C. March, M. March, C. March, M. March, M. March, M. March, M. March, C. March, M. Mar
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                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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   Rattus norvegicus (Norway rat)
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3 (bases 1 to 250470)
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Direct Submission
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COMMENT

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in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgum sequence reads. Both end sequences and whole genome shotgum sequence only contigs will be indicated in the feature table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AATTGGCAACTGTCTATTATCCATTCGGCAATCACATTTCGGATGTTCTCGAAAAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 240374 bases at least Q40 Consensus quality: 242949 bases at least Q30 Consensus quality: 245059 bases at least Q20 Consensus quality: 245059 bases at least Q20 Stimated insert size: 254162; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248046; contig of 248046 bp in length 248146; gap of unknown length 249193; contig of 1047 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249293: gap of unknown length 250470: contig of 1177 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH230-145E6
------ Summary Statistics
Assembly program: Atlas 3.0;
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GMMK
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1. .250470
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238284. .240199
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241389. .245579
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145250 ATATCGAAACTATTCTAGTGTTTTTGTCAAATTCTACTGAGAAAAGTATTTAGGGTTTAA 145191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (20-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 20, 2002 this sequence version replaced gi:18702446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 20-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (19-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                75 ATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTG 134
                                                                                                                                                                                                                                                                                                                  135 TGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC108074 110ear PRI 20-MA, Homo sapiens BAC clone RP11-717H13 from 4, complete sequence. AC108074 AC024668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                          Score 39; DB 2; Length 177864; Pred. No. 4.9; 0; Mismatches 75; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trani, L., Cotton, M., Creason, K. and Nguyen, C.
The sequence of Homo sapiens BAC clone RP11-717H13
                                                                                                                                                                                                                                                                                                                                                                                                                                             145130 Crcaraacaarcrcrrrrrrrrrrrrrrrgccaaaraaa 145092
                                                                                                                                                                                                                                                                                                                                                                                                     195 CTAGTAGTCAGTCAATAAATTCTACGTGGCAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 128635)
Sulstor,JE. and Weterston,R.
Toward a complete humar genome sequence
Genome Res. B (11), 1037-1108 (1998)
/note="assembly_name:Contigl5"
175174. .176585
/note="assembly_name:Contig7"
176686. .177864
                                                                                     /note="assembly_name:Contig9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0717H13
Drafting Center: WIBR
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2 (bases 1 to 128635)
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Waterston, R.H.
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5 (bases 1 to 128635)
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                                                                                                                                                   16,4%;
52,8%;
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                                                                                                                                                   Query Match
Best Local Similarity 52.83
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
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AC108074
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                                                               AC146595 177864 bp DNA linear HTG 06-SEP-2003
Mus musculus chromosome UNK clone RP24-164G18, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                              oummitted (06-SEP-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Czaniata, Vertebrata, Euteleostomî,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center Center code: WIGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1486: contig of 1486 bp in length
1586: gap of unknown length
24281: contig of 22695 bp in length
24381: gap of unknown length
660849: contig of 16468 bp in length
175073: contig of 114124 bp in length
175173: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 0$
Sequencing vector: Dismid, 10$
Sequencing vector: plasmid, 100$
Chemistry: Dye-primer ET; 0$ of reads
Chemistry: Dye-rerminator Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175803 bases at least Q1C
Consensus quality: 175803 bases at least Q2C
Consensus quality: 175912 bases at least Q2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length 177864: contig of 1179 bp in length. Location/Qualifiers
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gap of unknown length
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/note="assembly_name:Contigl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig12"
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/db xref="taxon:10090"
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/clone="RP24-164G18"
                                                                                                                                                   AC146595.1 GI:34494968
HTG; HTGS PHASE1.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 177864)
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60949:
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                              RESULT 9
AC146595/c
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                                                                        COCUS
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This sequence may not represent the entire insert of this
                                      clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subcione; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPhersor, Department of Genetics, Mashington University, St. Jouls MD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male conor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org JECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-384D10, 2000 bp overlap; the clone sequenced to the right is RP11-766L18. Actual start of this clone is at base position 21951 of RP11-384D10; actual end is at base position 128635 of RP11-717H13.

Data from AC027411 was used to finish this clone, AC108074.

The sequence of AC024668 has been incorporated into AC108074. Location/Qualifiers

organism="Homo sapiens" /mol_type="genomic_DNA" /db_xref="taxon:9606" clone="RP11-717H13" /clone_lib="RPCI-11" 7. .317 rpt_family="Alu" 100. 449 /rpt_family="52" chromosome="4" .128635 "map="4" repeat_region repeat_region repeat_region source FEATURES

746. ..811 / /rpt_family="(TA)n" 829. .1006 /rpt_family="(TA)n" 1007. .1030 rpt_family="AT_rich" 5422. .6079 /rpt_family="BRVL" 6486. .667° 6486. .6619 /rpt_family="ERVL" 8484. .864° 'rpt_family="(CA)n" 275. 1770 /rpt_family="MalR" 2046. .2066 'rpt_family="{A}n" 1093; .3133 rpt_family="ERVL" 'rpt_family="L1" .4324 repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

family="AT_rich" . .15008 family="AT_rich" family="AT_rich" . .15008 family≈"(TG)n" family="MalR" family="ERV1" family="L1"
8, .10904
family="L2"
1, .12211 family="Alu" . 14067 family="Alu" .2591€ family="Alu" 1. .21112 _family="L1" rpt family="L1" 7609. .27719 . ,23419 family="L1" . .24745 Family="L1" family="L1" family="L1" family="L1" /rpt_family="L1" 9152_ .10608 .13635 .20238 25029 .26213 .27013 .27471 .20932 /rpc_fa 24746. rpt_fa 720<u>6</u>. rpt_f 1135. rpt_f 0658. rpt f 4979 rpt_1 8551 0185. 0443 rpt_1 rpt f 5030. rpt_f 5937. rpt_f 6989. rpt_ 1911 1160 th. rpt rpt rpt rpt rpt, repeat_region repeat_region repeat region repeat_region repeat_region

family="AT_rich" family="(TTG)n" 3. .34316 _family="L1" 3. .34952 family="L1" I. .35154 rpt_family="L1" 2843. .34316 .30389 .32803 /rpt_fa 12127. rpt_fa 0364. 4453. rpt_f 5071 rpt. repeat_region repeat_region repeat_region repeat_region

family="MER2_type" 'rpt_family="AcHobo" 85233. .35457 family="L1" family="L1" .36083 .37520 rpt_f 5968. repeat_region repeat_region repeat_region repeat region repeat_region

37914. .38431 /note="match to EST AA809063 (NID:g2878469) nwl7al2.sl" 39777. 41891 /rpt_family="MER2_type" 43382. 45504 family="11" 3. .43308 family="L1" . .42231 family="12" family="Ll" family="īī" .43112 /rpt_family="] 46562. .46650 .43381 /rpt_f 43309. rpt_f 11892. /rpt_f 12388. /rpt_f 43108. repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature

repeat region

'rpt family="L2"

repeat_region

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Diblished Only in Database (2002)

Sasaki, T., Mateumoto, T. and Katayose, Y.

Sasaki, T., Mateumoto, T. and Katayose, Y.

Direct Submission

Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-860, Japan

E-mall:tasaaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

On Sep 25, 2003 this sequence version replaced gi:23200616.

The orientation of the sequence is from T7 to SP6 of the PAC clone.

Location/Qualifiers
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                                                                                             70260 rerchancaritreanacesesearararaseserritrancritrircriniacretri 70201
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Mus musculus chromosome UNK clone RP24-149E13, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
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                                                                                                                                                                                                                                                                                                                        APD05757 147655 bp DNA linear PLN 26-SEP-2003
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
PAC clone:P0413H11, ccmplete sequence.
                                             133 TGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Erreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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/organism=*Cryza sativa (japonica cultivar-group)"
/ordl_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="texaon:39947"
/clone="P0413H11"
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0413H11
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Indels
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42;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrhartoideae; Oryzeae; Oryza.
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AC132361.1 GI:22657848
                                                                                                                                                                                                                                                                                                                                                                                                              AP005757
AP005757.2 GI:35764583
     Conservative
     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
                                                                                                                                                                                                                                                                                     RESULT 12
AP005757/c
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TITLE
JOURNAL
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TITLE
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WOTE: It currently consists of 1 contigs. Gaps between the contrigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft, sequence."

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              118446 AGATTAAAATAATTTTTAAAATCAAGAAATTCTGGGAGCCAAAATGTTCAACTGGGA 118505
                                                                                                                                                                                                                                                                                                                                                                110386 CAATGAATTTCAACATATTGCAGAGGAAGGATTTCAGAATTTCATCAGAGAATTTAACAG 110445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) chromosome 8 clone P0518H02, *** SEQUENCING IN PROGRESS ***.
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                                                                                                                                                                                                                                                                                                                   81 CAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                141 AGTICGICAIGAAGITIACCCAAAGGACTITACTAIGIGAATTAAATTGICAAACTAGTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
1; Poales; Poaceae;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JAN-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
clone:P0518H02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Cryza sativa (japonica cultivar-group)"
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| cultivar="Nipponhare"
| db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.3%; Score 38.8; DB 2; Length 138772; 62.4%; Pred. No. 5.6;
                                                                                                                                                                                                           ch: 16.3%; Score 38.8; DB 9; Length 128635; I Similarity 55.1%; Pred. No. 5.7; 7; 76; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Speraryota, Viridiplantae, Streptophyta; Em
Spermatophyta, Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Only in Database (2002)
2 (bases 1 to 138772)
                                46753. .46938
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46884. .47008
/rpt_family="CT-rich"
46753. .46938
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                                                                                                        /rpt_family="(TA)n"
48559. .48780
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clone="P0516HC2"
                                                                                                                                                             'rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GTCAGATCAATAAAATTC 218
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KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

JOURNAL AUTHORS REFERENCE

REFERENCE

TITLE

COMMENT

RESULT 11 AP004700/c DEFINITION

Matches

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123078 GACTAGCAGTAATGCTAAGGGTTCCTAGTCAAGTGGAACAATAATTATGTTTTAAAG 123019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123018 TGCCAAGTCTGTATCAAAGGAATCAATAAAAACGTGGGAAGAAGATACACAAA 122961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TIACTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryofa, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Meoptera, Endopterygota, Diptera, Brachycera, Asilomorpha, Asiloidea, Therevidae, Stenogephrya.

1 (bases 1 to 1182)

Yang, L., Wiegmann, B.M., Yeates, D.K. and Irwin, M.E.
Highberlevel phylogeny of the Therevidae (Diptera: insecta) based on 28S ribosomal and elongation factor-1 alpha gene sequences
Mol. Phylogenet. Evol. 15 (3), 440-451 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ar14/831 1182 bp DNA linear INV 12
Stemogephrya sp. 288 ribosomal RNA gene, partial sequence.
AR147831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang.L., Wiegmann, B.M., Yeates, D.K. and Irwin, M.E.
Direct Submission
Submitted (03-My-1999) Entomology, North Carolina State
University, Box 7613, Raleigh, NC 27695, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.8; DB 2; Length 161010;
Pred. No. 5.6;
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16.3%; Score 38.8; DB 2; Length 16
Best Local Similarity 51.1%; Pred. No. 5.6;
Matches 91; Conservative 0; Mismatches 87; Indels
                                 1. .1984
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                                                                                                                                                                                                                                              // 15925, 15927
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159228, 161010
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68679. ,89216
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig19"
89317. .108734
/note="assembly_name:Contig20"
                                                                                                                     1264. .9331
/note="assembly_name:Contig12"
                                                                                                                                                                                                                            note="assembiy_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig17"
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/organism="Stenogephrya sp."
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                               53735. .68578
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Stenogephrya sp.
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                  Direct Submission
Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 161010)
MCPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 100$
Chemistry: Dye-primer ET; 0$ of reads
Chemistry: Dye-primer ET; 0$ of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 157791 bases at least 040
Consensus quality: 157791 bases at least 020
Consensus quality: 155407 bases at least 020
Insert size: 17520; agarose-fp
Insert size: 15990; sum-of-contigs
Quality coverage: 10.01 in 020 bases; agarose-fp
Quality coverage: 10.14 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40637: gap of unknown length 53534: contig of 12937 bp in length 53734: gap of unknown length 68578: contig of 14844 bp in length 68678: gap of unknown length 89216: contig of 20538 bp in length 89316: gap of unknown length 108734: contig of 19418 bp in length 108834: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1984: contig of 1584 bp in length
21084: gap of unknown length
4263: gap of unknown length
4263: gap of unknown length
9331: contig of 5068 bp in length
8431: gap of unknown length
16764: gap of unknown length
21118: contig of 733 bp in length
21118: contig of 4254 bp in length
30095: contig of 4854 bp in length
3195: gap of unknown length
3195: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159127: contig of 50293 bp in length
159227: gap of unknown length
161010: contig of 1783 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                             .----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 10342 bp in
                                                                                                                                                                                                                                                                                                                                                                               Center project name: M_BB0149B13
                                                                                                                                          2 [bases i to 161010)
McPherson, J.D. and Waterston, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1610:0
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                        ----- Genome Center
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/clone="RP24-149313"
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                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 132361 bases at least Q40 Consensus quality: 132381 bases at least Q30 Consensus quality: 132389 bases at least Q20 Insert size: 134000; aganose-fp Insert size: 134000; aganose-fp Qality coverage: 11.10x in Q20 bases; agarose-fp Quality coverage: 11.10x in Q20 bases; sum-of-contigs Quality coverage: 11.23x in Q20 bases; sum-of-contigs
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/note="clone overlaps with GenBank Accession Number
AC108193 clone RP86-469M8 (center project name coe)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced the finished sequence as soon as it is available and the finished sequence as soon as it is available and the accession number will be preserved.
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the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 38.6; DE Best Local Similarity 51.4%; Pred. No. 6.4; Matches 89; Conservative 0; Micmark-
                                                                                                                             with a Phrap-derived quality score.
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/note="assembly_fragment
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/mol_type="genomic DNA"
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/clone="RP86-44312"
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                                                                                                                                                                                                                                                                                                                                                          94 GATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 GABATTTTATAGAATTATTTTTATATAGTTTTTATTAAAGTAATTGAATTTGGTATGAC 343
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Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1. (bases 1 to 132389)
                                                                                                                                                                                                                                                                                                  34 GAIGCAACAGICTICTCTCCAATIGGCAACTGTCTAJIAICCAITCCGCAATCACAITICG 93
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Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 132389)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 GITTACCCAAAGGACTITACTATGIGAAFTAAATTGTCAAACTAGTAGTCAGA 206
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Pelis catus clone RP86-44312, WORKING DRAFT SEQUENCE.
AC108190
                                                                                                                                                                                                                                          Indels
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Center code: NISC
                                                                                                                                                                              16.2%; Score 38.6; DB 3; 51.4%; Pred, No. 9.7;
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/product="28S ribosomal RNA"
                                                                                                                                                                                                                                             0; Mismatches
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                          db_xref="taxon:95105"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Felis catus (cat)
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                                                                                                                                                                                                                                             89; Conservative
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Best Local Similarity
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LOCUS DEFINITION AC108190/c

ACCESSION KEYWORDS SOURCE

VERSION

RESULT 15

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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COMMENT

RFERENCE AUTHORS Search completed: July 7, 2004, 15:39:07 Job time: 1888 secs

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DB 2; Length 132389; 84; Indels

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2832.682 Million cell updates/sec
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                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Nicholas School of the Environment
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Box 90328, Durham, NC 27708-0328,
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/clone="DDRT26"
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J. Biol. Chem. 273 (48), 31962-31970 (1998)
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
1 (bases 1 to 933)
Liao, V. H. - C., and Freedman, J. H.
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                      /moi_type="mRNA"
/srrain="N2"
/db xref="taxon:6239"
/clone="DDRT16"
/tissue type="whole animal"
/dev stage="mixed population'
/clone_lib="mRNA from cadmium-responsive gene"
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organism="Caenorhabditis elegans"
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100.0%; Pred. No. 1.5e-45;
cive 0; Mismatches 0;
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/dev_stage="mixed population"
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Nicholas School of the Environment
Duke University
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/clone="DDRT16FC"
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238 bp mRNA linear EST 25-NOV-1998 AF071379 mRNA from cadmium-responsive gene Caenorhabditis elegans AP071379 ö 61 ACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAG 120 123 TIAITIGGAGTACTGGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 182 63 ACTGTCTATTATCCATTCCGCAATCACATTTCGGAATGTTCTCGAAAAGGACTTCCCAAAG 122 TTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180 183 1 TITITITITITITIGGGAGAAATCACGGCGGGATGCAACAGTCTTCTCTCTAATTGGCA 60 TTCTTTCGGGGGGGAGGAATCACGGCGGCGGACCAACAGTCTTCTCTCAATTGGCAACT 758 62 GICTAITAICCATICCGCAAICACATITCGGAIGTTCTCGAAAAGGACTICCCAAAGTIA 123 1 (bases I to 238)
Liao,V.H.-C. and Freedman,J.H.
Cadmium-regulated genes from the nematode Caenorhabditis elegans.
Identification and cloning of new cadmium-responsive genes by 3 TTTTTTTTTTGGGGAGGAATCACGGCTTCGGATGCAACAGTCTTCTCTCAATTGGCA 124 TIGGAGIACIGIGAAAGAGIICGICAIGAAGIIIACCCAAAGGACIIIACIAIGIGAAII Gaps .. /tissue_type="whole animal" /dev stage="mixed population" /clone_lib="mRNA from cadmium-responsive gene" Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. Length 238; Indels /organism="Caenorhabditis elegans" /mol type="mRNA" /strain="N2" differential display J. Biol. Chem. 273 (48), 31962-31970 (1998) 99041962 Score 223.2; DB 9; Pred. No. 4.2e-42; 8

rag.

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[ (Gases 1 to 511)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, S.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTS) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
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Cadmium-regulated genes from the nematode Caenorhabditis elegans. Identification and cloning of new cadmium-responsive genes by differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AANTCATGGGGGGGGGATGCAACAGTCT--TCTCAATTGGCAACTGTCTATAT--CATTCC
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9
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/dev stage="mixed population"
/clone lib="mRNA from cadmium-responsive gene"
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 214;
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                                                                                                                                                                                                                                                 1..214
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159; DB 9;
Pred. No. 4.6e-27;
0; Mismatches 5;
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                                                                                                                                                                                       Box 90328, Durham, NC 27708-0328, USA Email: jonf@duke.edu.
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Dana Farber Cancer Institute
4 Binney Street, Boston, MA 02115,
Tel: 617 632 5180
Fax: 617 632 2425
                                                                                                                                                     Nicholas School of the Environment
                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6239"
/clone="DDRT2"
                                                                                                                                Contact: Jonathan H. Freedman
                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 208; Conservative (
                                                                                                                                                                          Duke University
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BI175173/c
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                                                      217 bp mRNA linear EST 25-NOV-1998 AF071398 mRNA from cadmium-responsive gene Caenorhabditis elegans cJNA close DDRT7, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF071362 mRNA from cadmium-responsive gene Caenorhabditis elegans
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Liao, V.H.-C. and Freedman, J.H.
Cadmium.regulated geres from the nematode Caenorhabditis elegans.
Identification and cloning of new cadmium-responsive genes by
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/dev_stage="mixed population"
/clone_lib="mRNA from cadmium-responsive gene"
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                             differential display
J. Biol. Chem. 273 (48), 31962-31970 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Box 90328, Durham, NC 27708-0328, USA Email: jonf@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jonathan H. Freedman
Micholas School of the Environment
Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone DDRT2, mRNA sequence.
AF071362
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clone="DDRT7"
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Liao, V.H.-C. and Freedman, J.H.
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Caenorhabditis elegans
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EST 19-0CT-2000
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/tissue_type="whole animal"
/dev.stage="mixed stage"
/dev.stage="mixed stage"
/clone lib="AD-wrmcDNA library was generated with poly(A)+
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphredite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GICTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TATTTATTTGGASACCACATTGCTCCAGTTGATGCSACGGTTTTTAGCCAGTTGSCAGTT 117
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Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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AU115788 unpublished oligo-capped cDNA library Caenorhabditis
elegans CDNA clone yk/36g5 3', mRNA sequence.
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/clone_lib="unpublished oligo-capped cDNA library"
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Pred. No. 8.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 91; DB 14; Length 583; 70.8%; Pred. No. 2.2e-11;
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Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
                                                            organism="Caenorhabditis elegans"
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
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                                                                                       /mol_type="mRNA"
/strain="N2"
/db xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/strain="N2"
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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J. R., Harlbey, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chever, E., Papasotiropoulos, V.,
Tolias, P.P., Paccek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.I.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
purry vidal@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                  /dev_stage="mixed stage"
/clone_lib="mixed tymenDNA library was generated with poly(A)+
/note="Tipe AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDDAs by poly(A) priming. The
DDNAs were cloned into pPC86"
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Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans O cloning project : Contact jerome_reboul@dfci.harvard.edu or philippe_vaglio@dfci.harvard.edu
POLYM=No.
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Pred. No. 9.1e-20;
0; Mismatches 15; Indels U
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                                                                                                                                                                                      /organism="Caenorhabditis elegans"
|mol_type="mRNA"
/strain="N2"
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/tissue_type="whole animal"
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Marc Vidal Laboratory
Dana Farber Cancer Institute
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90.1%;
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Fax: 617 632 5739
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Best Local Similarity
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CB396141 567 bp mRNA linear EST 15-WAY-2003 OSTRE(58.1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence Lag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
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Bukaryota; Metazoa; Nematoda; Chromadorea; Khabditida;
Rhabditoidea; Rhabditidae; Peloderimae; Caenorhabditis.
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Pred. No. 2e-08;
0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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/mol_type="mRNA"
/strain="N2"
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/tissue_type="whole animal"
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marc_vidal@dfci.harvard.edu
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                                                                                                                                   IGTOTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTT 122
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MCCombie, W.R., Kelley, J.M., Aubin, L., Goscoechea, M.,
McCombie, W.R., Kelley, J.M., Adams, M.D., Dubnick, M., Kerlavage, A.R.,
Vencer, J. C. and Pields, C.A.
Caenorhabditis elegans CDNAs
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                                             190 TITCCIGITCGGAGACAAGAICACACGGGGAIGCAACAGIGIITGGICAAITGGGAAC
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/clone="CEESX27"
/clone_lib="Early embryo, Stratagene (cat. #937007)"
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Eukarycta; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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9712 Medical Center Drive, Rockville, MD 20850 USA
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /crganism="Caenorhabditis elegans"
  54;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
Email: arkerlav@tigr.org
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Contact: Kerlavage, AR
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Matches 144; Conserv
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    Matches
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T01925/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                    123 ATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTTACCCAAAGGACTTTACTATGTGAAT 182
                                                                                                                                                                                                       3 ITITITITITIGGGAGGAAALCACGGCGGGATCCAAACAGTCTTCTCTCAATTGGCAAC 62
                                                                                                                                                                                                                                                                                                                                                                             116 ILCTAACHACHINGIAACHGAACHBAACHGATAAAAGCAGTATHAAAGTCT 57
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/lofe lib="bog library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                   Query Match 17.1%; Score 40.8; DB 29; Length 636; Best Local Similarity 48.3%; Pred. No. 12; Matches 114; Conservative 0; Mismatches 122; Indels 0.
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Search completed: July 7, 2004, 16:21:39 Job time: 2513 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 7, 2004, 11:39:02 ; Search time 349 Seconds
(without alignments)
2897.052 Million cell updates/sec Run on:

JS-09-437-450A-40 score:

Perfect so Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues

Searched:

6747726

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:* 1: geneseqn1980s:* Database :

genesegn2001bs:* genesegn2003as:* geneseqn2001as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn1990s:* geneseqn2000s:* geneseqn2002s:* geneseon2004s: 8: 9: 10: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abv55254 Human pro	Abn80125 Human che	Aaa27331 Soybean p	Ach29861 Human tes	Aad16067 Soybean z	Abl33686 Human imm	Abl16740 Drosophil	Abx09781 M. incogn	Abg65781 Arabidops	Aak87745 Human dig	Aai57549 Human col	Abs99726 cDNA enco	Adb92806 Human col	Abl29872 Drosophil	Abq70819 Listeria		Abl29758 Drosophil	Human	Abl58167 Human glu	Abl34490 Human met	Abn80020 Human che	Abq67077 Human ang	Aal57561 Human mag
	di	ABV55254	ABN80125	AAA27331	ACH29861	AAD16067	ABL33686	ABL16740	ABX09781	ABQ65781	AAK87745	AAI57549	ABS99726	ADB92806	ABL29872	ABQ70819	ABL02096	ABL29758	ABQ67094	ABL58167	ABL34490	ABN80020	AB067077	AAL57561
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	Score	34.6	34.6	33.6	33.4	33.4	33.2	33	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.8	32.6	32.6	32.6	32.6	32.4
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ALIGNMENTS

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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                         Human prostate expression marker cDMA 55245.
ABV55254 standard; cDNA; 199 BP
                                                                                                                                      17-FBB-2000; 2C00US-0183319P.
16-MAR-2000; 2C00US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021914P.
18-UUL-2000; 2000US-0255281P.
                                                                                                                         20-FEB-2001; 2001WO-US005171.
                            (first entry)
                                                                                             W0200160860-A2.
                                                                                Homo sapiens.
                                                                                                           23-AUG-2001.
                            17-SEP-2002
             ABV55254;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Monahan JE; Endege WO, Schlegel R,

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 10673; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing

229

Indels

59;

55;

Best Loca Matches

ð Вb 8

Query Match

8888888

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Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or [11] and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, [17] and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on pequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                  110 ACTTOCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamine amidotransferase; histidine biosynthesis; herbicide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides encoding plant glutamine amidotransferase homologs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 TTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAA
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                                                                                                                                                                                                                                                          Score 34.6; DB 6; Length 6036;
Pred. No. 6.4;
                                                                                                                                                                                                              Sequence 6036 BP; 1473 A; 98 C; 1516 G; 2949 T; 0 U; 0 Other;
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/transl_except= {pos:275.
/note= "Xaa=unknown"
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Best Local Similarity 54.3
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-376564/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism.
       the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                  150 TGAAGITIACCCAAAGGACTITACTAIGTGAATTAAATIGECAAACTAGTAGTCAGAICA 209
                                                                                                                                                                                                                                                                                                                                                            57 TGCAGGATACACAATTGACACAAAAAGGAAAATAATAAAGCCAAACTGGTATTCAAAAA 116
                                                                                                                                                                                                                                                                      0; Gaps
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heart disease; epilepsy; histone deacetylation; muscular dystrophy;
dwarfism; single nuclectide polymorphism; SNF; cytosine methylation;
antidiabetic; cytostatic; anticonvulsant; ds.
                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human chemically modified disease associated gene SEQ ID NO 142.
                                                                                                                                                                                                                      Length 199;
                                                                                                                                                                                                                                                                    34; Indels
                                                                                                                                                                            Sequence 199 3P, 105 A, 34 C, 37 G, 22 T, 0 U; 1 Other;
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Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
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61.8%;
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                                                                                                                                                                                                                                                   Local Similarity
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Homo sapiens.

Synthetic.

03-JAN-2002

15-JUL-2002

ABN80125;

셤

.277, aa:Xaa)

The present sequence is a Glycine max (soybean) putative glutamine amidotransferase coding sequence. The protein forms a crucial stage in

development.

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AAD16067 standard; cDNA; 1208
                                                                                                                         14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00461474.
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                                                                                                                                                                                                                                                                                                                                                  339 AAAAAAAAAAAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Eirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product=
                                                                                                                                                  Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                           226 CAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
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P-PSDB; AAE09323.
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS.
                                                                                                                                                                                                                                                                          166
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD16067;
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S_ycine
                                                                                                                                                                                                                                                                                                                                                                                                    AAD16067/c
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the histidine biosynthesis pathway. The sequence can be used to create transgenic plants which express different amounts of the protein, to identify loss of function mutants and to produce the protein in a host cell, for example a bacterium. The protein can be used to identify inhibitors which may be useful as functiones and herbicides. The gene was identified by computer screening for sequences which could encode
                                                                                                                                                                            143 TICGICALGAAGITIACCCAAAGGACTITACTATGIGAATTAAATTGICAAACTAGIAGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                Human, ss, sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping, biodiversity, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA libraries, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one of
                                                                                                                                                                                                   572 Trigiaaratititaagaaaarararitiaccargiigcagcactarcrcrgaacaritist 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide comprising any one of 18543 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome and gene
or in generating
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones LW;
                                                                                                                            DB 3; Length 671;
                                                                                                     Sequence 671 BF; 217 A; 104 C; 144 G; 205 T; 0 U; 1 Other;
                                                                                                                                                    39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein,
                                                                                                                                                                                                                             203 CAGATCAATAAATTCTACGTGGCAAAAAAAAAA 238
                                                                                                                                                                                                                                                    632 TATTACAAATTATTTCATGTGTCAAAAAAAAAA 667
                                                                                                                            Score 33.6; Di
Pred. No. 6.4;
                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 17073; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stache-Crain B,
                                                                                                                                                                                                                                                                                                                 ACH29861 standard; cDNA; 404 BP
                                                                             histidine biosynthetic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00918995.
                                                                                                                              14.1%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                      57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                          Human testis cDNA #247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense DNA or RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615964/58.
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JONES
                                                                                                                                                                                                                                                                                                                                                                  13-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2003.
                                                                                                                                                                                                                                                                                                                                         ACH29861;
                                                                                                                              Query Match
                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRIGA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LABA/
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Matches
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for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was sequained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AAGGACTICCCAAAGITATIGGAGIACTGIGAAAGAGIICGICAIGAAGITTACCCAAAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 AAAATTTGAACATTTTAGTTCTTGGTTATAAAATGTTAATTCAGAA--TTAGTTTAAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACTITACTATGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GCCTTAATTAAACTAATTAATAGCTTTGGACACTTAAAAGAGCTCTAAATTTGCCTTGTAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New arsenic transporter polypeptides and polynucleotides, useful for
producing transgenic plants with altered level of heavy metal tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 ITCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; soybean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean zinc transporter (ZnT-2) cDNA from clone se6.pk0012.h2:fis.
                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  t= "Soybean zinc transporter protein" "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                         Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                       Sequence 404 BP; 143 A; 43 C; 77 G; 137 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                     Score 33.4; DB Fed. No. 6.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporter; zinc transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΕΙ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Col 41-42; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Gaps

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Indels

53;

BP.

DB 6; Length 8781;

Score 33.2; DB Pred. No. 19; 0; Mismatches

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anamnia, cancer, acute myeloid leukaemia, Albainer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                     121 TIATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                   191 iraiataataacittattattatetataiaaraacitiftatataaataacittatiaiheta 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polymucleotide SEQ ID NO 1693.
                                                                                                                                                                                                                          Sequence 8781 BP; 2407 A; 65 C; 2093 G; 4216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL16740 standard; DNA; 20693
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                                                                                                                                                                                                                                                                                  13.9%;
                                                                                                                                                                                                                                                                                                      55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171042-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                  65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL16740;
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL16740/c
                                                                                                                                                                                                                                                                                                                                  Matches
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                 The invention relates to heavy metal (e.g. arsemite and zinc) transporter polypeptides and polymediates. The polypeptides of the invention are useful for producing antibodies that are useful for screening CDNA expression libraries to isolate full length clones of interest. The antibodies are also useful for detecting the polypeptides in situ, in cells or in vitro, in cell extracts. Nucleic acid molecules of the invention are useful for producing transgenic plants with altered tolerance to heavy metals. They are also useful as probes for genetically and physically mapping the genes. The trans a part of, and as markers for traits linked to those genes. The present sequence is soybean zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGAC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 TICCCAAAGITATIGGAGIACIGIGAAAGAGITICGICAIGAAGIITACCCAAAGGACTIT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804 Triccadariningeadeargricangingicoccaracarriacidadargarrag 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, immune system disease, cytosine methylation, antiasthmatic; antiarchiselercitic, antiamenho; cytostatic; nootropic; antiamenho; cytostatic; nootropic; anti-INV, anticonvulsant, ophthalmological; antirhermatic; antiarchito; antidiabetic; antipsoriatic; antiinflammatory; eye disease; arcerlosclerosis; anaemia; antiinflammatory; eye disease; arcerlosclerosis; anaemia; authinflammatorid; sheamer's disease; AlDS; epilepsy; neurofibromatosis; rhenamatorid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       864 CAACAGCCCCCTTTCAAGCTTAGTAGCATCTATCTCACGAGGTGTGTTCTCCATCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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O
                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1208;
                                                                                                                                                                                                                                                                                                              Sequence 1208 BP; 347 A; 208 C; 281 G; 372 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1659.
                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                           Score 33.4; Dl
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                transporter (ZnT-2) protein cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33686 standard, DNA; 8781 BP.
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2000DB-01043826.
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                                                                                                                                                                                                                                                                                                                                                              14.0%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ACT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 AGT 742
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation.
                                                                                                                                                                                                                                                                                                                                                                                                            : 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
ABL33666/C
1D ASL3366/C
1D 26-MARS
XX ABL336
DT 26-MARS
XX Human;
KW Human;
KW ABLICH
K
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of inserticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG175 ABLIG175, ABLIG175, and the encoded proteins (ABB7737-BBR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
New isolated mucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                  claim 1; SEQ ID NO 1693; 21pp + Sequence Listing; English.
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Page A, Mathew AV,
Kricker M, Slater T,
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                                                                                                                                                                                                                                                       49; Conservative
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MATHEW A V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GARCIA C A.
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DAVIS K R.
ALLEN K.
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(PAGE/)
(MATH/)
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(HAAS/)
(GARC/)
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                                                                                                                                                                11638 ATTICCAATGATTAATCCTITGATACGTATTCACCTTTTGGTGTTTTCCCATATGTATAT 11579
                                                                                                                                                                                                                                                                                  11578 TCCAAATACATTTCAATTGGTCCTCAAAGTGGTTCGGTAATATCCCCAAATATGCATTAC 11519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA mediated interference molecule useful for disrupting cellular process in a nematode, for controlling nematodes comprises genetic regulatory
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                                                                                                              113
                                                                                                                                                                                                                         114 CCCAAAGTIATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTAC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to RNAi (double-stranded interfering RNA or
                                                                                                                                                                                                                                                                                                                                                                                    11518 CATCACCATTITAAATGAATACTACTIGTCCGGAAACACAAAAGGTTAAATGGAAA 11462
                                                                                                                                                                                                                                                                                                                                       174 TATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA mediated interference; mRNA transcript, nematode gene; growth; development; parasitism; reproduction; RNAi vector; mRNA translation; nematode inhibitor; agricultural industry; anti-nematode; ds.
                                                                                                           54 ATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTT
                                                        Gaps
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  Length 20693;
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                                                        Indels
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DB 4; ]
Score 33; DB 4, Pred. No. 28; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX09781 standard; DNA; 571 BF.
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  13.9%;
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                                                        87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease; stress; metabolic patcway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.
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produce nematode inhibitors or RNAi in the plants, and provide new biorechnological strategies for managing nematodes under sustainable agricultural conditions. ABX09677-ABX09815 represent RNAi molecules useful for the control of nematodes
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Hoffman N;
                                                                                                                                                                                                                                 DB 6; Length 571;
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Ledford BL, Woessner
, Davis KR, Allen K,
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2000US-C246475P.
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25-SEP-2000;
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08-NOV-2000;
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The invention relates to nucleic acids (1) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their fragments. (1) are used to express the corresponding polyperides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/blosynthetic pathways (for production of commercial, or untritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics), Note: The sequence data for this patent did not form part of the printed specification, but was obtained in sequence construction of the printed by 1999 of 1999 o
                                                                                                                                                                                                                                                                                                                                                                   AAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, digestive system antigen, gene therapy, cancer, appendicitis, ulcerative colitis, infection, Hirschsprung's disease, chronic colitis, digestive system disorder, Meckel's diverticulum; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auman digestive system antigen coding sequence SEQ ID NO: 61.
                                                                                                                                                                                                                                                                                                  Score 32.8; DB 6; Length 678;
Pred. No. 11;
                                                                                                                                                                                                                                                                    Segmence 678 BP; 161 A; 198 C; 110 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                    27; Indels
                               Claim 1; SEQ ID NO 358; 40pp + Sequence Listing; English
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13.8%; Score 32.8; Discal Similarity 64.5%; Pred. No. 11;
les 49; Conservative 0; Mismatches
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18-ARR-2000; 2000US-019123P.
19-MAY-2000; 2000US-0209467P.
07-UIN-2000; 2000US-021488F.
38-UIN-2000; 2000US-021488F.
07-UIL-2003; 2000US-02155P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 223 TGGCAAAAAAAAA 238
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24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-WAR-2000; 2000US-018934P.
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 altered metabolism.
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AAX87745/c
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108 AGAIGATITTAGGGACATITTATTTTTATAAATTTACAATCTAATGGTNANAAAAAA 49
                                                                                                                                                                                                                                                                                                Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                                                                                                                                                                                                 Human colorectal cancer antigen cDNA SEQ ID NO: 13.
                                                   213 AAATTCTACGTGGCAAAAAAAAAA 238
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2000US-0205515P.
2000US-0209467P.
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2000US-0226868P.
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01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
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2000US-0228963P.
                                                                                                                                                                   AAI57549 standard; cDNA; 745
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2000US-0184664P.
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30-JUN-2000; 2
C7-JUL-2000; 2
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14-AUG-2000;
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22-AUG-2000;
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ID AAI575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides encoding digestive system antigens, useful
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17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
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17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-02519P.
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2000US-0246610P.
2000US-0246611P.
2000US-0246611P.
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2000US-024920P.
2000US-024920P.
2000US-0249210P.
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2000US-C246528P.
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Best Local Similarity
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05-JAN-2001;

Matches

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72-0CT-2000; 2000US-023/03/F.

72-0CT-2000; 2000US-023/03/F.

72-0CT-2000; 2000US-023/03/F.

73-0CT-2000; 2000US-023/03/F.

73-0CT-2000; 2000US-023/93/F.

73-0CT-2000; 2000US-024/93/F.

70-0CT-2000; 2000US-024/13/F.

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08-NOV-2000; 2000US-0246609P.

08-NOV-2000; 2000US-0246610P.

08-NOV-2000; 2000US-0246611P.

17-NOV-2000; 2000US-0246613P.

17-NOV-2000; 2000US-0246613P.
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08-NOV-2000; 2000US-0246524P.
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08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
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2000US-0249214P.
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2000US-0233065P.
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                           08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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17-NOV-2000;
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                                                                                                         14-SEP-2000;
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The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAL57547-AAL57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 AGTITACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTAGTCGGATCAATA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AGATGATTTTAGGGACATTTTATTTTAAATTTACAATCTAATGGTNANAAAAAAA 49
                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis.
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Pred. No. 11;
0; Mismatches 34; Indels (
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ID ABS99726 standard; cDNA; 745 BP.
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08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-025199P.
05-JAN-2001; 2001US-025679P.
                                         2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
2000US-0251988P.
2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
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Best Local Similarity 60.5%,
Thes 52; Conservative
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P-PSDB; AAM38571.
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17-NOV-2000; 2
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05-DBC-2000; 2
06-DBC-2000; 2
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musculoskeletal system disorder; Albers-Schonberg disease;
Marfan's syndrome; neurological disease; phenylketonuria;
Mernicke's encephalogathy; Alzheimer's disease; endocrine disorder;
Grave's disease; Cushing's syndrome; reproductive system disorder;
prostatosis; benign prostatic hypertrophy; benign prostatic hyperplasia;
thrombosis; atherosclerosis; myocardial infarction; ischaemic attack.
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17-MAR-2020; 2000US-0190076P.
18-APR-2020; 2000US-0198123P.
19-MAY-2020; 2000US-0205515P.
07-UJM-2020; 2000US-0209467P.
28-JUN-2020; 2000US-0214886P.
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08-SEP-2000; 2000US-0231244P.
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2000US-0218290P.
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                                                                                                              Homo sapiens.
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08-SEP-2000;
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    The present invention relates to the isolation of novel human colorectal cancer related proteins, and polymucleotide sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of the calon and/or rectum, including colorectal cancer. Colorectal cancer metastases, and gastrointestical disorders such as dysphagia, peptic oesophagitis, gastric reflux, colorectal cancer metastases, and gastrointestical disorders such as dysphagia, peptic oesophagitis, gastric reflux, colorectal syndrome, and peritoneal diseases. The invention also describes antibodies that bind colorectal cancer related polymolectic methods for producing unman colorectal cancer related polymolectices, polypeptides, and/or antibodies. MBS99724-ABS99796 represent cDNA sequence encoding human colorectal cancer related proceins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPFO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AGTITACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAATA 212
                                                                                                                                                                                                                                                       New colorectal cancer polypeptide for diagnosing, prognosing, preventing, and treating immune, hyperproliferative, liver, kidney, reproductive disorders and for identifying modulators of therapeutic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AGAIGATITIAGGGACATITITATITITAAATITAAATITIACAATCIAATGGINANAAAAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptic ulcer, Bruton's disease, X linked infantile agammaglobulinaemia, severe colbined immunodeficiency, DiGeorge anomaly, hyperproliferative disorder; acute lymphoblastic leukaemia, acute lymphocytic leukaemia, rinnary system disorder; cortical necrosis; kidney infarction, cardinovascular disorder; carcinoid heart disease, arrhythmia; respiratory disorder; non-allergic rhinitis; simusitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; gene; human; cclorectal cancer; antigen; gene therapy; gastrointestinal disorder; inflammatory disease; infection; cancer; intestinal neoplasm; small intestine carcinoid tumour;
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                                                                                                                                                                                                           WPI; 2002-731367/79.
                                                                                                              (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                      29-BUG-2002
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05-DEC-2000; 2000US-0251030P.
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06-DEC-2000; 2000US-025149P.
06-DEC-2000; 2000US-025149P.
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08-DEC-2000; 2000US-0251868P.
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                                                                 2000US-0234997P.
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2000US-0235484P.
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20-OCT-2000; 20c0US-0241809P.
0-OCT-2000; 20c0US-02481826P.
01-NOV-2000; 20c0US-0244617P.
08-NOV-2000; 20c0US-024647P.
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The invention relates to a colorectal cancer antigen. The antigen is useful for chromosome identification, chromosome mapping, radiation by brid ampping or gene therapy, or as hybridisation probes for alferential identification of the tissues or cell types present in a differential identification of the tissues or cell types present in a colorical sample. The antigen is useful for treating, preventing, inflammatory diseases and/or conditions, infections, cancers (e.g. inflammatory diseases and/or conditions, infections, cancers (e.g. intetinal neoplasms (carcinoid tumour of the small intestine, normal edgkin's lymphoma of the small intestine, small bowel lymphoma) and uncers (e.g. peptic ulcers). The antigen and its mucleic acid are useful corprovide immunological probes for differential identification of the cissue. The antigen and its mucleic acid are useful for treating, preventing, diagnosing and/or prognosing diseases, disorders and/or conditions of the immune system e.g. Bruton's disease, X linked infantile agammaglobulinaemia, severe combined immunodeficiencies, Diceorge concerning and/or diagnosing hyperproliferative disorders (e.g. acute preventing and/or diagnosing hyperproliferative disorders (e.g. acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 AGITTACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
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                                                                                                                                                                                                                                                            Novel colorectal cancer antigen useful for treating, preventing, diagnosing and/or prognosing gastrointestinal disorders, infections, cancers such as intestinal neoplasms, ulcers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 41089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.8%; Score 32.8; DB 9; Length 745; llarity 60.5%; Pred. No. 11; Conservative 0; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 дадададададададададада 23
                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 13; 179pp; English
                                                                                                                                                             Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL29872 standard, DNA; 2630 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-C0614150.
08-DEC-2000; 2000US-0251989P-

08-DEC-2000; 2000US-0251990P-

11-DEC-2000; 2000US-0254097P-

CS-JAN-2001; 2001US-0259578P-

17-JAN-2001; 2001US-0259578F-
                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
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                                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 52; Conserva
                                                                                                                                                                                                     WPI; 2003-708345/67.
                                                                                                                                                                                                                        P-PSDB; ADB92879.
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                                                                                                                                                                 Rosen CA,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL04640-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 ATCACATITCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 CHATCAGTHATGATATGCTAAAATGGTATTGTCATHCATTGAGTTTAAAAAAA 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 TCACGGCGGCGGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCA
                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 ITCGTCATGAAGTITACCCAAAGGACTITACTATGTGAATTAAATTGTCAAA 194
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                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 41089; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes 4b contig DNA sequence #761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 32.8;
                                                                                 Myers BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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                                                                              PWD,
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(first entry)
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(CNRS ) CNRS CENT NAT
                                                                              Adams M,
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                                                                                                                                WPI; 2001-656860/75
                         (PEKE ) PE CORP NY.
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29-AUG-2002
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                                                                                 Wenter JC,
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114 A897
27 A80
29 A90
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New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.

K Claim 14; SEQ ID NO 3632; 180pp; French.
The present invention relates to nucleic acid sequences (ABQ67188-
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The present invention relates to nucleic acid sequences (ABG67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. and contaminants in foods, or mutational analysis) and for analysis of gene expression. Proceins encoded by the rucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antifisteria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at frow. Whipo.inf.pub/published.pct.sequences. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 3423 BP; 1040 A; 693 C; 620 G; 1070 T; 0 U; 0 Other;

Query Match 13.8%; Score 32.8; DB 6; Length 3423; Best Local Similarity 59.8%; Pred. No. 18; Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps

0

Qy 118 AAGTTATTGGAGTACTGTGAAAGAGTTCGTCA 149
Db 2437 CACATCTGGGARAGTAGAAATGTTTCGGCA 2468

barch completed: July 7, 2004, 15:07:29
bb time : 353 secs

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1630.596 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 11, Appli Sequence 213, Ap Sequence 213, Ap Sequence 3, Appli Sequence 3, Appli Sequence 38, Appli Sequence 38, Appli Sequence 149, Appl Sequence 149, Appli Sequence 149, Appli Sequence 266, Appli Sequence 101, App Sequence 91, Appl Sequence 93, Appl Sequence 91, Appl Appli Appl Appl 1, App Sequence 1, Ag Sequence 10, 7 Sequence 99, 7 Sequence 101, Sequence 99, 7 Description Sequence 2 Sequence 2 US-09-461-474-11 US-09-621-976-2813 US-08-870-518-7 US-08-870-518-7 US-08-13-419B-3 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-477-38 US-09-511-87-89 US-09-601-198-145 US-09-601-198-145 US-09-601-198-145 US-09-601-198-146 US-09-601-198-146 US-09-601-198-166 US-09-601-101 US-09-601-101 US-09-322-409-91 US-09-322-409-91 US-09-322-409-91 US-09-322-409-93 US-08-313-608B-2 SUMMARIES DB 640681 738 1269 1269 1269 1369 1302 4 1302 477 696 4 2244 4 1664976 Length 5183 6124 29793 29793 29793 401 401 401 401 Query Match 1 13.52 13.52 13.52 13.52 13.52 13.53 14.0 Score υ O Ç)

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	US-09-833-381-1759	4	1287	12.0	12	28.6	4		
Sequence 117, App	US-09-489-847-117	4	3338	12.1	77	28.8	4	υ	
222(US-09-134-000C-2226	4	2163	12.2	12	29	42		
Sequence 362, App	JS-09-134-001C-362	4	666	7	12	29	4		
Sequence 1400, Ap	JS-C9-540-236-1400	4	243	12.2	12	20	40	Ü	
Sequence 1, Appli	US-09-643-990A-1	4	1830121	m.	12	29.3	39		
	US-09-557-884-1	4	1830121	ų	2	29.3	38		
Sequence 5, Appli	JS-09-152-406-5	m	2322	m.	12	29.3	37		
Seguence 1, Appli	JS-09-152-406-1	m	2322	'n	12	29.5	36	υ	
Seguence 6, Appli	US-09-444-336-6	4	1465	12.4	12	29.4	35		
Seguence 22, Appl	US-08-724-394A-22	ď	246240	12,4	12	29.6	34		
Seguence 21, Appl	US-08-724-394A-21	N	246240	12.4	12	29.6	33		
Seguence 20, Appl	US-08-724-394A-20	2	246240	541 	2	29.6	32		
Seguence 1, Appli	US-08-459-324-1	7	479	12.4	77	29.6	31		
Seguence 1, Appli	US-08-313-608B-1	Н	479	12.4	12	29.6	30		
Sequence 3599, Ap	US-09-107-532A-3599	4	477	₩.	12	29.6	23		
Sequence 2, Appli	US-08-459-324-2	7	477	4	12	29.6	28	υ	

ALIGNMENTS

RESULT 1

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Patent No. 6287570
GENERAL INFORMITION:
GENERAL INFORMITION:
TITLE OF INVENTION: Vaccine Against Swine Influenza
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 2509
                                                                                                                                FILE REFERENCE: BB1301 US NA
FILE REFERENCE: BB1301 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
RARLIER PLING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 17
SEQ ID NOS: 17
SEQ ID NO 11
          Sequence 11, Application US/09461474
Patent No. 6278042
                                                                        APPLICANT: Allen, Steve
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 67, Conserv
                                                       GENERAL INFORMATION:
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US-09-461-474-11/c
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                                                                                  175 MANGKKWWRYATTWRRAMMWWAAWTMMWYMWWAWCMSSRCAAMYRRTMMWGYRYWWRK 116
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235 IWCYNYWXYWKAMWSKICWSGSRGGYMISYISIRSYSMYWASWWKYIMCWWWGRWWSIYWY 176
                                            67 TAT--TATCCATICCGCAATCACATITCGGATGTTCTCGGAAAGGACTTCCCAAAGTTAT 124
                                                                                                                             125 TGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTA 184
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ITACIATGEGRATTAAATTGECAAACTAGEGAGAGATGAATAAAAITGEAGG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5183;
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Davis, Roger J.
APPLICANT: Davis, Roger J.
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows95
SOFTWARE: EsstSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION VUMBER: US/08/870,513
FILING DATE: 06-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31.6; DE
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04020/102001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08870518
; Patent No. 5925566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 5183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 617/542-5070
617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fasse, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 85; Conserva'
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                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-870-518-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   US-08-870-518-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TITITITIGGGAGGAAATCACGGCGGCGGAAGCAACTGTCTCTCTCAATTGGCAACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AAATCACGGCGGCGGATGCAACAGTCTTCTCTCTAATTGGCAACTGTCTATTATCCATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1646 scharcheriterechicheciecharecertinach 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jobert, S. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REPRENCE: GENSET 054PR2. CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.4; DB 3;
Pred, No. 1.3;
0; Mismatches 41;
                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/197,679A
FILING DATE: 23-NO. 628/570-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative 112; Mismatches
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REFERENCE/DOCKET NUMBER: foley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-8405
TELEFAX: (703) 425-8406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1724 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.68;
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Conservative
                               STATE: Virginia
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                         ZIP: 22031
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Best Local Similarity
Matches 57; Conserv
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 235..399
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US-09-621-976-2813/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-621-976-2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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TITE OF INVENTION: GENER ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG)
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES INMUNORBACT
TITLE OF INVENTION: THEREMITH
FILE REFERENCE: NIAD 201
CURRENT APPLICATION NUMBER: US/09/511,477
CURRENT PILING DATE: 2000-223
PRIOR APPLICATION NUMBER: 09/302,812
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                            21128 TITITICCCATTARAGIGAATICARARATATITIATICICATATSCTIGGITCTAGTARATT 21069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21188 GAITITICIACATTCCIATIGCCAACGAIGTITTCAALAATGTTAATGAAATTTTCTTGTT 21129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21128 TİTİTCCCATTAAAGIGAATİCAAAATATİTTAİTİĞİCATATGCTİGGİTCTAGIAATT 21069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 GITTACCCAAAGGACTITACTAIGIGAATIAAAIIGICAAACTAGIAGICAGAICAAIAA 213
                                                                                                                                                                                                                                        94 GAIGITCTCGAAAAGGACTICCCAAAGITATIGGAGIACIGIGAAAGAGIICGTCAIGAA 153
                                                                                                                                                                                                                                                                                                                                          154 GITTACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTAGTCGGATCAATAA 213
                                                                                                                                                                                                                                                                                          21188 dairirichacarrecrarreccaaceargrirreaaraardraararrirricrierr
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                                                                                                                                      13.2%; Score 31.4; DB 4; Length 29793; liarity 51.0%; Pred. No. 7.8; Conservative 0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 13.2%; Score 31.4; DB 4; Similarity 51.0%; Pred. No. 7.8; 74; Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21068 TTTAATTTTTGAAAAAAAAAAA 21044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21068 TITAATITITIGAAAAAAAAAAA 21044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AATTCTACGTGGCAAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 AATTCTACGTGGCAAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/09511507; Patent No. 6395543; GENERAL INFORMATION: APPLICANT: JACOBSON, Myron K. APPLICANT: JACOBSON, Blaine L. APPLICANT: AME, Jean-Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38, Application US/09511477
Patent No. 6337202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Caenorhabaditis elegans
                     TYPE: DNA ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: JACOBSON, Myron K.
APPLICANT: JACOBSON, Elaine L.
APPLICANT: AME, Jean-Christophe
APPLICANT: LIN, Winston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 38
                                                                                                                                         Query Match
Best Local Similarity
Matches 74; Conservat
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Matches 74; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-511-477-38/c
                                                                       ; FEATURE:
US-09-302-812-38
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LENGTH: 297
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APELICANT: CACCOBON, Elaine L.
APELICANT: CACCOBON, Elaine L.
APELICANT: ACCOBON, Elaine L.
APELICANT: ACCOBON, Elaine L.
APELICANT: M. Winston
TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENTITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES INMUNOREACTIVE
TITLE OF INVENTION: THERMITH
FILLS OF INVENTION: THERMITH
FILLS OF INVENTION NUMBER: US/09/302,812B
CURRENT PILLNG DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,768
EARLIER PILLNG DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Inselburg, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       865 CATGALACCTICCATTICGIAAATGGAAATTATTITTICCATAATGALATATAATA 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 TICICGAAAAGGACTICCCAAAGITATIGGAGIACTGIGAAAGAGITGGICATGAAGITT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 ACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTAGTAGTCAGATCAATAAAATT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CAACAGICITCICICAAIIGGCAACIGTCIAITAICCAITCCGCAAICACAITICGGAIG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
3900 GIMITATGSCAGATGAGATGGGACTTGGTAAGACACTTCAATGTATTGCTTTGT 3953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%; Score 31.4; DB 4; Length 6124; 47.3%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                          FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/09302812B
Patent No. 6333148
GENERAL INFORMATION:
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                                                                                            78-08-213-419B-3/c
; Sequence 3, Application US/08213419B
: Patent No. 6333406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYPE: DNA ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.38
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (2598)..(3404)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (3580)..(3720)
NAME/KEY: CDS
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LENGTH: 6124
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278 AIGCITITIAAAATCCWAAACTAATATCAGTAGCCATGGAGTCATCGGCTTGAGG 219
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Pred. No. 2.2;
1; Mismatches 69; Indels
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EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
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                                                                                          EARLIER FILING DATE: 1397-07-08
EARLIER APPLICATION UNBER: 60/051,928
EARLIER APPLICATION UNBER: 60/055,722
EARLIER APPLICATION UNBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
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OTHER INFORMATION: n equals a,t,g, or c
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SARLIER FILING DATE: 1997-08-18
SARLIER PLICATION NUMBER: 60,055,984
EARLIER FILING DATE: 1997-08-18
EARLIER PILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/055,947
FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
                                          APPLICATION NUMBER: 60/051,919
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FILING DATE: 1997-08-18
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OTHER INFORMATION: n equals a,t,g,
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Patentin Ver. 2.0
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Best Local Similarity 50.74
Matches 72; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (605)
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APPLICANT: LIN, Winston
TITLE OF INVENTION: GENES BNCODING SEVERAL FOLY (ADP-RIBOSE) GLYCCHYDROLASE (PARG) EN
TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNORBACTIV
TITLE OF INVENTION: THEREWITH
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Best Local Similarity 51.0%; Pred. No. 7.8;
Matches 74; Conservative 0; Mismatches 71; Indels 0;
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FILE REFERENCE: F2012P1
CURRENT PAPLICATION NUMBER: US/09/227,357
CURRENT PAPLICATION NUMBER: US/09/227,357
CURRENT PAPLICATION NUMBER: PCT/US98/13684
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1999-01-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
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CURRENT APPLICATION NUMBER: US/09/511,507
CURRENT FILING DATE: 2000-02-23
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APPLICATION NUMBER: 60/052,795
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Patent No. 6342581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Caenorhabaditis elegans
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APPLICANT: Fischer et al.
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US-09-511-507-38
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NAME/KET: misc feature
LOCATION: (309398)...(309398)
NAME/KET: misc feature
LOCATION: (309398)...(309398)
NAME/KET: misc feature
LOCATION: (309418)...(309418)
NOTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (312837)...(312837)
NOTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (312993)...(312993)
OTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (319226)...(319226)
OTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (319226)...(319226)
OTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (319286)...(319216)
OTHER INFORMATION: nequals a, r, c, or g
NAME/KET: misc feature
LOCATION: (559167)...(559167)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: {98239}..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t,
                                                                NAME/KBY: misc_feature_
LOCATION: (98120). (98120)
OTHER INPORMATION: n equals a, t,
NAME/KBY: misc_feature
LOCATION: (98159). (98159)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
COATION: (234220)...(234220)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
                     LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a, NAME/KEY: misc feature
LOCATION: (500992)..(600992)
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OTHER INFORMATION: n equals a,
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misc_feature
(84812)..(848
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APPLICANT: Bult et al.

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729

TITLE OF INVENTION: jannaschii

FILE REFERENCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,4218

FIRM APPLICATION NUMBER: US/08/924,428

PRIOR FILING DATE: 1997-06-22

NUMBER: OF SEQ ID NOS: 3
                                                                                                           GENERAL INFORMATION:
APPLICANT: Casel). Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Heiner, Chery? R.
APPLICANT: Heiner, Chery? R.
APPLICANT: Heiner, Chery? R.
APPLICANT: Lefkowitz, Eliot
TITLE OF INVENTION: UNCLEIC ACID PROBES AND METHOD FOR DETECTING URRAPLASMA,
TITLE OF INVENTION: URB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 200-12-08
PRICE PRILING DATE: 1999-01-30
PRICE FILING DATE: 1999-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 TICGGAIGIICICGGAAAAGGACTICCCAAAGIIATIGGAGTACTGTGAAAGAGTICGICA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 TGAAGTTTACCCAAAGGACTTTACTATGAATTAAATTGTCAAAC 195
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LOCATION: (28222). (28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KET: misc feature
LOCATION: (28257). (28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LCCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LCCATION: (84868). (848688)
OTHER INFORMATION: n equals a, t, c, or g
                                                                Sequence 149, Application US/09601198
Patent No. 6531583
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US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
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SEQ 1D NO 1
LENGTH: 1664976
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 181
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Best Local Similarity
Matches 59; Conservē
                                                  CS-09-601-198-149
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                                                                                                                                                                                                                                                                                                                                                                          619728 AATGATAAATTTTAGTCTACGAACGTTCTATCAAGATGATATTATAAAAACTACA 619672
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                                                                                   1 TITITITITITITIGGGAGGAATCACGGCGGCGGATGCAACAGTCTTCTCTCAATTGGCA
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12.9%; Score 30.5; DB 4; Length 1664976; 45.6%; Pred. No. 56; Live 0; Mismatches 129; Indels 0; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 CAGATCAATAAATTCTACGTGGCAAAAAAAA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 266, Application US/09643597; Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(401); OTHER INFORMATION: n = A,T,C or G US-09-643-597-266
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Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
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Best Local Similarity 49.787
...thes 76, Conservative
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Li, Samuel X.
Wang, Aijun
                                             108; Conservative
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                        Best Local Similarity
Matches 108; Conserva
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US-09-643-597-266/c
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        Query Match
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RESULT 13 US-09-480-884A-266/c

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83 ATCACATTTCGGAJGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 7, 2004, 16:22:46 Job time : 87 secs
                                                                                                                                                                                                                                                                                                                                                           Sequence 266, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(401)
CTHER INFORMATION: n = A,T,C or G
US-09-606-421B-266
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Railos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Garger, Garg R.
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.74
Matches 76; Conservative
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ORGANISM: Homo sapien
FEATURE:
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12.8%; Score 30.4; DB 4; Length 401;
Best Local Similarity 49.7%; Pred. No. 3.1;
Matches 76; Conservative 0; Mismatches 77; Indels
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Sequence 266, Application US/09542615A

Patent No. 6218256

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Ran, Ligun

APPLICANT: Ran, Ligun

APPLICANT: Rangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: APPLICANT: Nancy A.

APPLICANT: APPLICANT: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF LUNG CANCER

FILE REPERENCE: 210121.455C8

CURRENT FILING DAIRS: 200-04-14

NUMBER OF SEQ ID NOS: 350

SOPTHARE: FASTEED for Windows Version 3.0
                                                                APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liquin
APPLICANT: Hosken, Nancy A.
APPLICANT: Alos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: CANDONNON: CANDONNON AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
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CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DAIE: 2001-08-27
WHMBER OF SEQ ID NGS: 330
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 266
Sequence 266, Application US/09480884A Patent No. 6482597
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i OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-266
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| OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-266
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Best Local Similarity 49.7
Matches 75, Conservative
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
                                             GENERAL INFORMATION:
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US-09-542-615A-266/c
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181 ATTACAAAATGATTGATTTAAAGAATTTTTAAAATCCAGAAGTCATTAAAATAG 122
                                                                         143 ITCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGT 202
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                                                                                                                                          121 BACCICATATAGTATGAACHATAAAATATTTTACATTTCATGAAARTTTTGCTGT 62
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
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July 7, 2004, 15:01:33 ; Search time 344 Seconds (without alignments) 3337.679 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpna/PCT_NBW_PUBL.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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238
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	ĽB	ID	Description
-	37	15.5	į	13	US-10-085-783A-49714	Sequence 49714, A
7	37	15.5		16	US-10-242-535A-49714	Sequence 49714, A
m	36.2	15.2	•	12	US-10-041-018-135	Sequence 135, App
4	34.2	14.4		13	US-10-424-599-87084	Sequence B7384, A
. 2	34.2	14.4	614	13	US-10-027-632-94282	Sequence 94282, A
9	34.2	14.4		13	US-10-027-632-305384	Sequence 305384,
7	34.2	14.4		16	US-10-027-632-94282	Sequence 94282, A
σο	34.2	14.4		16	US-10-027-632-305384	Sequence 305384,
σ	33.4	14.0		10	US-09-918-995-17073	Sequence 17373, A
01 0	33.4	14.0		o,	US-09-783-590-5790	Sequence 5750, Ap
11	33.2	13.9	~	15	US-10-311-455-1659	Sequence 1659, Ap
12	32.8	13.8		g	US-09-770-149-358	Sequence 358, App
13	32.8	13.8		Φ	US-09-764-855-13	Sequence 13, Appl
14	32.B	13.8		15	US-10-072-349-13	Segmence 13. Appl

16 US-10-398-221-36 15 US-10-342-887-76 13 US-10-342-8887-76 13 US-10-172-118-76 15 US-10-175-523-61 15 US-10-175-523-61 15 US-10-175-523-61 15 US-10-175-523-61 15 US-10-175-523-61 16 US-10-027-632-22 17 US-09-938-842A-4 11 US-09-938-842A-4 11 US-09-938-842A-4 11 US-09-938-842A-4 11 US-09-938-842A-4 11 US-10-21-714A-1 12 US-09-938-842A-4 13 US-09-938-842A-4 14 US-09-938-842A-4 15 US-09-938-842A-4 16 US-09-938-842A-4 17 US-10-21-714A-1 18 US-09-938-842A-4 19 US-09-938-842A-4 10 US-09-938-842A-4 11 US-10-106-698-88 12 US-09-973-278-878 13 US-09-973-278-878 14 US-10-311-455-12 15 US-10-311-455-12 16 US-10-318-493-451-38 18 US-09-997-32-12	363	43	Sequence 765, App	Sequence 765, App	Sequence 440, App	58,	61,	Seguence 79,	Sequence 86,	Sequence 2242		c)	Seguence 4562, Ap	٠,	Seguence 289, App	Segmence 5, Appli	111	188	Sequence 589, App	37	Sequence 455	5	873,	Sequence 30, Appl	Sequence 12	Sequence	Sequence	Sequence 4210	Seguence 44	Sequence 121, App	Sequence 38, Appl
15 32.8 13.8 3423 1 1 1 1 1 1 1 1 1	US-10-398-221-3632	US-10-240-485-43	US-10-342-887-765	US-10-172-118-765	US-10-311-455-440		US-10-175-523-61		. US-10-074-475-86	US-10-027-632-22426	US-10-027-632-22426	US-09-938-842A-4562	. US-09-938-842A-4562	US-10-221-714A-187	US-09-997-722-289	US-09-844-653-5	US-10-021-323-5635	US-09-814-353-18833	. US-10-106-698-589			US-09-973-278-872	US-09-973-278-873	US-08-927-939-30						-722-1	US-09-973-451-38
15 32.8 16 32.8 17 32.8 18 32.4 13.5 20 32.2 2 13.5 20 32	1423 16	5117 15	698 13	698 13	3373 15	٦	364 15	Н	133 15	607 13	91 209	6 0007	11 0003	5565 13	5597 12	850 10	506 17	644 10	778 15	Н	Н	2034 13	2787 13	1259 8	H		Ä	Ä	Н	5083 12	1793 9
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SULT 1 **10-085-783A-49714 **201-085-783A-49714 **201-085-783A-49714 **201-085-783A **201-085-783A-49714 **201-085-783A-49714	h Similarity 52.2%; Pred. No. 0.77; 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;	TGGCAACTGTCTATTATCCATTCCGCAACCACATTTCGGATGTTCTCGAAAAGGACTTCC 115	CAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTA	109 CTTIGCCTTGATAGAATIGTAACAICAIGCTCCAAGAATATAAATTCCAATAATTTACTA 168
114, 49714 114, Application of the property of	g	TGGCAACTGTCT	CAAAGTTATTGG	CITTGCCTTGATA
RESULT 1 US-10-085-783A-49714 Sequence 49714, Appl Publication No. US20, GENERAL INFORMATION: APPLICANT: Chondrod APPLICANT: Liew, C TITLE OF INVENTION: FILE REFERENCE: 423 CURRENT APPLICATION CURRENT FILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: PRIOR FLILING DATE: NUMBER OF SEQ ID NO SOFTWARE: PATENTIN SEQ ID NO 49714 LENGTH: 263 TYPE: DNA URGANISM: Human US-10-085-783A-49714	Query Match Best Local Similarity Matches 82; Conser	Oy 56 7		109 pp

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US-10-027-632-94282/c
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Matches 57
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TITLE OF INVEXTUON: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT FILING DATE: 2002-09-12
RICH APPLICATION NUMBER: US/10/242,335A
FILING DATE: 2002-09-12
RICH RILING DATE: 2002-09-13
PRIOR PLILING DATE: 2004-09-13
PRIOR PLILING DATE: 2004-09-13
PRIOR PLILING DATE: 2004-09-13
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PRIOR PLILING DATE: 2004-09-13
PRIOR RILING DATE: 2004-09-13
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PRIOR RILING DATE: 2004-09-12
PRIOR PLILING DATE: 2004-09-12
PRIOR FILING DATE: 2004-09-12
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PRIOR PLILING DATE: 2004-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135, Application US/10041018
Publication No. US2004007223A1
CENRRAL INFORMATION:
APPLICANT: Matsuda, Seiichi P.T.
ITLE PO INVERTION: Ditexpene-Producing Unicellular Organism
FILE REFERENCE: P02080US1/10025547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Indels
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176 TGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
                               169 TAAAASTAAATTTTAAAACTTTATGTTAAATTAACA 205
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Best Local Similarity 55.0%; Pred. No. 4.8;
Matches 71; Conservative 0; Mismatches 58;
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CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/25980
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ 1D NOS: 413
SOFTWARE: Patentin version 3.1
                                                                                                                                                       ; Sequence 49714, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
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ORGANISM: Gossypium hirsutum
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Best Local Similarity
Matches 82; Conserv
                                                                                                              RESULT 2
US-10-242-535A-49714
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ORGANISM: Human
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Sequence 87084, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Acad Income J
APPLICANT: Caco Yongwei
TITLE OF INVENTION: SO Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SO Nucleic Acid Molecules and Other Molecules Associated Mith
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
FURNER OF SEQ ID NOS: 285684
                           144 TCGTCATGAAGTITACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTAGTC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 ITGIGATATGGTTAAGAAAATATATTTACCATGTGCAGCACTATCTCTGAACATTTGTT 116
110 ACTICCCAAAGITATIGGAGIACIGIGAAAGAGITCGICAIGAAGITTACCCAAAGGACT 169
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Pred. No. 5.6;
C; Mismatches 38; Indels 0.
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_49647C.1
US-10-424-599-87084
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57; Conservative
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                                                                                                                                                                                                    356 AAATAAAA 364
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ORGANISM: Glycine max
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TYPE: DNA
ORGANISM: Human
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                                                                                                                                   Length 614;
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                                                                                                                                   14.4%; Score 34.2; DB 13; Length 64.6%; Pred. No. 7.7; tive 0; Mismatches 28; Indels
PRIOR APPLICATION NUMBER: US 60/146,002
PATOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 94282
                                                                                                                                                                                                                                                                                                                                        Sequence 305384, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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US-10-027-632-94282/c
; Sequence 94282, Application US/10027632
; Publication No. US20030204075A9
                                                                                                                                                                                                                                             220 ACGTGGCAAAAAAAAA 238
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Best Local Similarity 64.64
Matches 51; Conservative
                                                                                                                                                              51; Conservative
                                                                                                                                                 Best Local Similarity
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US-10-027-632-305384/c
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                                                                                            ORGANISM: Fuman
                                                                                                         US-10-027-632-94282
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                                                                               DNA
                                                                                                                                   Query Match
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CURRENT APPLICATION NUMBER: US/09/783,590
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LOCATION: (395)
OTHER INFORMATICN: n equals a,t,g, or c
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                        CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR PPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12465
SCFTWARE: Patentin Ver. 2.0
ISSC ID NO 5790
LENGTH: 499
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CTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                    160 CCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTGAGATCAATAAAATTCT 219
                                                                                                                                                                                    46 ITCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 AAAAATTTGAACATTTTAGTTCTTGGTTATAAAAATGTTAATTCAGAA--TTAGTTTAAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 GRCTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 GCCTTAATTAACTAATTAATAGCTTTGGACACTTAAAAGAGCTCTAAATTTGCTTGTAA 338
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APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
ITILE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REPERROCE: PO-16.2C1
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                             14.4%; Score 34.2; DE 16; Length 614; 64.6%; Pred. No. 7.7; ive 0; Mismatches 28; Indels 0;
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14.0%; Score 33.4; DB 10; Length 404;
Best Local Similarity 51.8%; Pred. No. 11;
Matches 100; Conservative 0; Mismatches 91; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-918-995-17073

) Sequence 11073, Application US/09918955

; Requence 11073, Application US/09918955

; Publication No. US20030073623A1

; GENERAL INPORATION:

/ APPLICANT: Hyseq, Inc.

/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

: TITLE OF INVENTION: PROM VARIOUS CONA LIBERRIES

: TITLE REPERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

; RICK FILING DATE: 1999-01-20

; NUMBER OF FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE FEASTSEQ FOR WINGONS VERSION 3.0
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Patent No. US20020110850A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | LOCATION: (1).T.(404)
| OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17073
                                                                                                                                                                                                                                                        220 ACGTGGCRAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                        120 ATGTGACAACAAAACAGA 102
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                          Query Match
Best Local Similarity 64.6%
The State Sign Conservative
The State Sign Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 CAAAAAAAAAA 238
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-09-783-590-5790/c
US-10-027-632-305384
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Publication No. US20030143606Al
GENERAL INFCRMATION:
APPLICANT: PLEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete:
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Dete:
TITLE OF INVENTION: DIAGNOSIS 2013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EPD1/07537
PRIOR APPLICATION NUMBER: PCT/EPD1/07537
PRIOR PELING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
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PRIOR PLING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ATTANATIGICANACTAGIAGICAGAICAATANAATTCTACGIGGCAAAAAAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
CHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8781;
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APPLICANT: Allen, Keith R.
APPLICANT: Allen, Keith Neil APPLICANT: Hurban, Neil APPLICANT: Hurban, Patrick TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: thaliam FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/170,149
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 13.9%; Score 33.2; DB 15;
1 Similarity 55.1%; Pred. No. 52;
65; Conservative 0; Mismatches 53;
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SOFFWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 358
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 358, Application US/09770149
Patent No. US2002659653A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
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Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page, Amy
Matthew, Abraham V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu, Yang
Rameaka, Joshua G.
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Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 65; Conserv
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US-09-770-149-358/c
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 CTACTAATAACNCCAAAATNAAATTTAATAACTCTACTACAGGAGCTTNCCACTTTTTCA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 GGAGTACTGTGAAAGAGTTCGTCATGAAGTTTTACCCAAAGGACTTTACTATGTGAATTAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 TAAGTIGITANCAACATITITGGGTTATTCAGAACATCTAACAGCATGTTCTAA 162
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14.0%; Score 33.4; DB 9; Length 499;
Best Local Similarity 50.3%; Pred. No. 12;
Matches 76; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 ATTGTCAAACTAGTAGTCAGATCAATAAAT 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or c
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US-10-311-455-1659/c
; Sequence 1659, Application US/10311455
                                                                                         LOCATION: (398)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (408)
OTHER INFORMATION: n equals a,t,g,
                        LOCATION: (396)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (439)
OTHER INFORMATION: n equals a,t,g,
NAME/XEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                               LOCATION: (423)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (470)
OTESE INFORMATION: n equals a,t,g,
NANE/KEY: misc feature
                                                                                                                                                                                                                                         LOCATION: (417)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (438)
OTHER INFORMATION: n equals a,t,g,
NAME/XEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (476)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
    WAME/KEY: misc feature
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NAME/KEY: misc feature
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LOCATION: (492)
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                                                                             NAME/KEY: misc feature
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US-10-072-349-13
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                                                                                                                                                       163 AAGGACTITIACTATGTGAATTAAATTGTCAAACTAGTAGTCGATCAATAAAATTCTACG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 AGITTACCCAAAGGACTITACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 ATCHARGITITHARGIGGITIGAGITOTAATACTISCIGITIGCALAATAAATGITIG
                                                                                                                  Gaps
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                                                                        13.8%; Score 32.8; DB 9; Length 678; ilarity 64.5%; Pred. No. 21; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 13.8%; Score 32.8; DB 9; Length 745; Similarity 60.5%; Pred. No. 22; 52; Conservative C; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAIN.
CURRENT APPLICATION NUMBER: US/09/764,855
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: n equals a,t,g, or G
NAME/KEY: SITE
LOCATION: (56)
DIFFRE INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09764855
Patent No. US20020119919A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                 223 TGGCAAAAAAAAA 238
                                                                                                                                                                                                                                                                    23 TAGTTAAAAAAAA 8
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FEATURE:
                                                                                        Best_Local Similarity
Matches 49; Conserv
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Matches 52; Conserv
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US-09-764-855-13/c
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LOCATION: (587)
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LOCATION: (711)
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                                      US-09-770-149-358
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                                                                            Query Match
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RESULT 14 US-10-072-349-13/c

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153 AGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATA 212
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; Publication No. US20640018514A1
; Publication No. US20640018514A1
; GENREAL INPORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: KUNST, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REPREACE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2000-10-04
; NUMBER: OF SEQ ID NOS: 4025
; SOGTWARE: PatentIn version 3.0
; SEQ ID NO 3632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.8; DB 15; Length 745;
Pred. No. 22;
0; Mismatches 34; Indels 0;
                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PALIOCI
CURRENT APPLICATION UNBER: US/10/072,349
CURRENT FILING DATE: 2002-02-11
Prior Application removed - See file Wrapper or Palm
NUMBER: OF EQ. ID NOS: 334
SOCTWARE: Patentin Ver. 3.1
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (397)
OTHER INFORMATION: n equals a,t,g, or NAME/KER: misc_feature
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Sequence 13, Application US/10072349
Publication No. US20030054420A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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Matches 52; Conserv
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US-10-398-221-3632
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### FEATURE:
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